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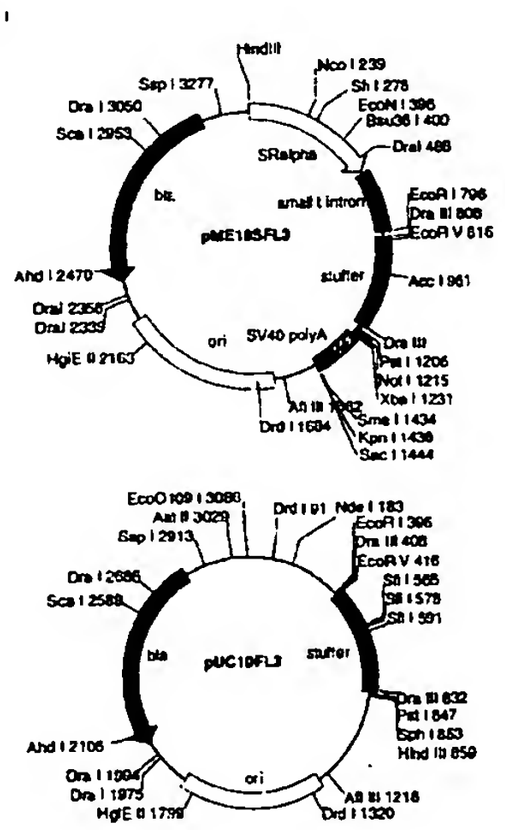
Remarks:
The sequence listing, which is published as annex to the application documents, was filed after the date of filing. The applicant has declared that it does not include matter which goes beyond the content of the application as filed.

(54) Primers for synthesizing full length cDNA clones and their use

(57) Primers for synthesizing full length cDNAs and their use are provided.

830 cDNA encoding a human protein has been isolated and nucleotide sequences of 5'-, and 3'-ends of the cDNA have been determined. Furthermore, primers for synthesizing the full length cDNA have been provided to clarify the function of the protein encoded by the cDNA. The full length cDNA of the present invention containing the translation start site provides information useful for analyzing the functions of the protein.

Figure 1



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EP 1 130 094 A2

Description

FIELD OF THE INVENTION

[0001] The present invention relates to a polynucleotide encoding a novel protein, a protein encoded by the polynucleotide, and new uses of these.

BACKGROUND OF THE INVENTION

[0002] Currently, the sequencing projects, the determination and analysis of the genomic DNA of various living organisms have been in progress all over the world. The whole genomic sequences of more than 10 species of prokaryotes, a lower eukaryote, yeast, and a multicellular eukaryote, C. elegans are already determined. As to human genome, which is supposed to be composed of three thousand million base pairs, the world wide cooperative projects have been under way to analyze it, and the whole structure is predicted to be determined by the years 2002-2003. The aim of the determination of genomic sequence is to reveal the functions of all genes and their regulation and to understand living organisms as a network of interactions between genes, proteins, cells or individuals through deducing the information in a genome, which is a blueprint of the highly complicated living organisms. To understand living organisms by utilizing the genomic information from various species is not only important as an academic subject, but also socially significant from the viewpoint of industrial application.

[0003] However, determination of genomic sequences itself cannnot identify the functions of all genes. For example, as for yeast, only the function of approximately half of the 6000 genes, which is predicted based on the genomic sequence, was able to be deduced. As for human, the number of the genes is predicted to be approximately one hundred thousand. Therefore, it is desirable to establish "a high throughput analysis system of the gene functions" which allows us to identify rapidly and efficiently the functions of vast amounts of the genes obtained by the genomic sequencing.

[0004] Many genes in the eukaryotic genome are split by introns into multiple exons. Thus, it is difficult to predict correctly the structure of encoded protein solely based on genomic information. In contrast, cDNA, which is produced from mRNA that lacks introns, encodes a protein as a single continuous amino acid sequence and allows us to identify the primary structure of the protein easily. In human cDNA research, to date, more than one million ESTs (Expression Sequence Tags) are publicly available, and the ESTs presumably cover not less than 80% of all human genes.

[0005] The information of ESTs is utilized for analyzing the structure of human genome, or for predicting the exon-regions of genomic sequences or their expression profile. However, many human ESTs have been derived from proximal regions to the 3'-end of cDNA, and information around the 5'-end of mRNA is extremely little. Among these human cDNAs, the number of the corresponding mRNAs whose encoding protein sequences are deduced is approximately 7000, and further, the number of full-length therein is only 5500. Thus, even including cDNA registered as EST, the percentage of human cDNA obtained so far is estimated to be 10-15% of all the genes.

[0006] It is possible to identify the transcription start site of mRNA on the genomic sequence based on the 5'-end sequence of a full-length cDNA, and to analyze factors involved in the stability of mRNA that is contained in the cDNA, or in its regulation of expression at the translation stage. Also, since a full-length cDNA contains ATG, the translation start site, in the 5'-region, it can be translated into a protein in a correct frame. Therefore, it is possible to produce a large amount of the protein encoded by the cDNA or to analyze biological activity of the expressed protein by utilizing an appropriate expression system. Thus, analysis of a full-length cDNA provides valuable information which complements the information from genome sequencing. Also, full-length cDNA clones that can be expressed are extremely valuable in empirical analysis of gene function and in industrial application.

[0007] In particular, human secretory proteins or membrane proteins are would be useful by itself as a medicine like tissue plasminogen activator (TPA), or as a target of medicines like membrane receptors. In addition, genes for signal transduction-associated proteins (protein kinases, etc.), glycoprotein-associated proteins, transcription-associated proteins, and disease-associated proteins form a gene group rich in genes whose relationships to human diseases have been elucidated.

[0008] Therefore, it has great significance to isolate novel full-length cDNA clones of human, only few of which has been isolated. Especially, isolation of a novel cDNA clone encoding a secretory protein or membrane protein is desired since the protein itself would be useful as a medicine, and also the clones potentially include a gene associated with diseases. In addition, genes encoding proteins that are associated with signal transduction, glycoprotein, transcription, or diseases are expected to be useful as target molecules for therapy, or as medicines themselves. These genes form a gene group predicted to be strongly associated with diseases. Thus, identification of the full-length cDNA clones encoding those proteins has great significance.

SUMMARY OF THE INVENTION

[0009] An objective of the present invention is to provide a primer that enables synthesizing polynucleotide from human, the resulting polynucleotide or its clone, and a protein encoded by the polynucleotide.

[0010] The inventors have developed a method for efficiently cloning a human full-length cDNA that is predicted by the ATGpr etc. to be a full-length cDNA clone, from a full-length-enriched cDNA library that is synthesized by the oligo-capping method. Then, the inventors determined the nucleotide sequence of the obtained cDNA clones from both 5'- and 3'- ends. By utilizing the sequences, the inventors selected clones that were expected to contain a signal by the PSORT (Nakai K. and Kanehisa M. (1992) Genomics 14: 897-911), and obtained clones that contain a cDNA encoding a secretory protein or membrane protein. Moreover, the inventors specifically selected full-length cDNA clones that encode secretory or membrane proteins, signal transduction-associated proteins, glycoprotein-associated proteins, transcription-associated proteins, or disease-associated proteins from clones homologous to the clones in the Swiss-Prot (http://www.ebi.ac.uk/ebi_docsSwissProt_db/swisshome.html) according to the keywords of SwissProt.

[0011] The full-length cDNA clones of the present invention have high fullness ratio since these were obtained by the combination of (1) construction of a full-length-enriched cDNA library that is synthesized by the oligo-capping method, and (2) a system in which fullness ratio is evaluated from the nucleotide sequence of the 5'-end (in this system, clones are selected based on the estimation by the ATGpr, following the removal of sequences judged not to be full-length when compared with ESTs). However, the primers of the present invention enable obtaining full-length cDNA easily without any special methods mentioned above.

[0012] Homology analysis in which the analysis is carried out against a non-full-length cDNA fragment to postulate the function of a protein encoded by said fragment, is being commonly performed. However, since such analysis is based on the information of the fragment, it is not clear as to whether this fragment corresponds to a part that is functionally important in the protein. In other words, the reliability of the homology analysis based on the information of a fragment is doubtful, as information relating to the structure of the whole protein is not available. However, the homology analysis of the present invention is conducted based on the information of a full-length cDNA comprising the whole coding region of the cDNA, and therefore, the homology of various portions of the protein can be analyzed. Hence, the reliability of the homology analysis has been dramatically improved in the present invention.

[0013] The inventors completed the invention by finding that it is possible to synthesize a novel full-length cDNA by using the combination of a primer that is designed based on the nucleotide sequence of the 5'-ends of the selected full-length cDNA clones and any of an oligo-dT primer or a 3'-primer that is designed based on the nucleotide sequence of the 3'-ends of the selected clones.

[0014] Thus, the present invention relates to primers described below, a method for synthesizing a polynucleotide using the primers, and polynucleotides obtained by the method.

[0015] First, the present invention relates to

(1) use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-829 and 2545, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides;

(2) a primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-829 and 2545, wherein said oligonucleotide comprises at least 15 nucleotides; and

(3) A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide comprising a nuclectide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence / 3'-end nucleotide sequence is selected from the combinations of 5'-end nucleotide sequence / 3'-end nucleotide sequence set forth in the SEQ ID NOs in Table 1.

[0016] Table 1 shows names of clones obtained in the examples described later, comprising the polynucleotide of the present invention (830 clones), names of nucleotide sequences at the 5'-end and 3'-end of the full-length cDNA, and their corresponding SEQ ID NOs. A blank indicates that the of the 3'-end sequence corresponding to the 5'-end sequence has not been determined the same clone.

[0017] The SEQ ID NO of a 5'-end sequence is shown on the right side of the name of the 5'-end sequence, and the SEQ ID NO of a 3'-end sequence is shown on the right side of the name of the 3'-end sequence.

Table 1

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
BNGH41000020	F-BNGH41000020	1		
BNGH41000087	F-BNGH41000087	2		
BNGH41000091	F-BNGH41000091	3		
HEMBA1000006	F-HEMBA1000006	4	R-HEMBA1000006	830
HEMBA1000121	F-HEMBA1000121	5	R-HEMBA1000121	831
HEMBA1000128	F-HEMBA1000128	6	R-HEMBA1000128	832
HEMBA1000275	F-HEMBA1000275	7	R-HEMBA1000275	833
HEMBA1000300	F-HEMBA1000300	8	R-HEMBA1000300	834
HEMBA1000349	F-HEMBA1000349	9	R-nnnnnnnnnnnn	835
HEMBA1000443	F-HEMBA1000443	10		
HEMBA1000462	F-HEMBA1000462	11	R-HEMBA1000462	836
HEMBA1000477	F-HEMBA1000477	12	R-HEMBA1000477	837
HEMBA1000590	F-HEMBA1000590	13	R-HEMBA1000590	838
HEMBA1000634	F-HEMBA1000634	14	R-HEMBA1000634	839
HEMBA1000671	F-HEMBA1000671	15	R-HEMBA1000671	840
HEMBA1000713	F-HEMBA1000713	16	R-HEMBA1000713	841
HEMBA1000732	F-HEMBA1000732	17	R-HEMBA1000732	842
HEMBA1000745	F-HEMBA1000745	18	R-nnnnnnnnnnnn	843
HEMBA1000835	F-HEMBA1000835	19		
HEMBA1000875	F-HEMBA1000875	20	R-HEMBA1000875	844
HEMBA1000907	F-HEMBA1000907	21		
HEMBA1000940	F-HEMBA1000940	22	R-HEMBA1000940	845
HEMBA1000962	F-HEMBA1000962	23	R-HEMBA1000962	846
HEMBA1001184	F-HEMBA1001184	24	R-HEMBA1001184	847
HEMBA1001221	F-HEMBA1001221	25	R-HEMBA1001221	848
HEMBA1001228	F-HEMBA1001228	26	R-HEMBA1001228	849
HEMBA1001272	F-HEMBA1001272	27	R-HEMBA1001272	850
HEMBA1001296	F-HEMBA1001296	28	R-HEMBA1001296	851
HEMBA1001297	F-HEMBA1001297	29	R-HEMBA1001297	852
HEMBA1001390	F-HEMBA1001390	30	R-HEMBA1001390	853
HEMBA1001563	F-HEMBA1001563	31	R-HEMBA1001563	854
HEMBA1001621	F-HEMBA1001621	32	R-HEMBA1001621	855
HEMBA1001878	F-HEMBA1001878	33	R-HEMBA1001878	856
HEMBA1001886	F-HEMBA1001886	34	R-HEMBA1001886	857
HEMBA1002048	F-HEMBA1002048	35	R-HEMBA1002048	858
HEMBA1002131	F-HEMBA1002131	36	R-HEMBA1002131	859
HEMBA1002163	F-HEMBA1002163	37	R-HEMBA1002163	860
HEMBA1002164	F-HEMBA1002164	38		
HEMBA1002167	F-HEMBA1002167	39	R-HEMBA1002167	861
HEMBA1002178	F-HEMBA1002178	40	R-HEMBA1002178	862
HEMBA1002195	F-HEMBA1002195	41	R-HEMBA1002195	863
HEMBA1002227	F-HEMBA1002227	42	R-HEMBA1002227	864
HEMBA1002239	F-HEMBA1002239	43		
HEMBA1002316	F-HEMBA1002316	44	R-HEMBA1002316	865
HEMBA1002420	F-HEMBA1002420	45	R-HEMBA1002420	866
HEMBA1002421	F-HEMBA1002421	46	R-HEMBA1002421	867
HEMBA1002524	F-HEMBA1002524	47	R-HEMBA1002524	868

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
HEMBA1002551	F-HEMBA1002551	48	R-HEMBA1002551	869
HEMBA1002767	F-HEMBA1002767	49	R-HEMBA1002767	870
HEMBA1002985	F-HEMBA1002985	50	R-HEMBA1002985	871
HEMBA1002992	F-HEMBA1002992	51		
HEMBA1003047	F-HEMBA1003047	52	R-HEMBA1003047	872
HEMBA1003072	F-HEMBA1003072	53	R-HEMBA1003072	873
HEMBA1003101	F-HEMBA1003101	54	R-HEMBA1003101	874
HEMBA1003120	F-HEMBA1003120	55	R-HEMBA1003120	875
HEMBA1003230	F-HEMBA1003230	56	R-HEMBA1003230	876
HEMBA1003294	F-HEMBA1003294	57	R-HEMBA1003294	877
HEMBA1003315	F-HEMBA1003315	58	R-HEMBA1003315	878
HEMBA1003392	F-HEMBA1003392	59	R-HEMBA1003392	879
HEMBA1003399	F-HEMBA1003399	60	R-HEMBA1003399	880
HEMBA1003487	F-HEMBA1003487	61	R-HEMBA1003487	881
HEMBA1003497	F-HEMBA1003497	62	R-HEMBA1003497	882
HEMBA1003530	F-HEMBA1003530	63	R-HEMBA1003530	883
HEMBA1003602	F-HEMBA1003602	64	R-HEMBA1003602	884
HEMBA1003732	F-HEMBA1003732	65	R-HEMBA1003732	885
HEMBA1003945	F-HEMBA1003945	66	R-HEMBA1003945	886
HEMBA1004007	F-HEMBA1004007	67	R-HEMBA1004007	887
HEMBA1004067	F-HEMBA1004067	68		
HEMBA1004085	F-HEMBA1004085	69	R-HEMBA1004085	888
HEMBA1004110	F-HEMBA1004110	70	R-nnnnnnnnnnnn	889
HEMBA1004250	F-HEMBA1004250	71	R-HEMBA1004250	890
HEMBA1004391	F-HEMBA1004391	72	R-HEMBA1004391	891
HEMBA1004444	F-HEMBA1004444	73	R-HEMBA1004444	892
HEMBA1004454	F-HEMBA1004454	74	R-HEMBA1004454	893
HEMBA1004505	F-HEMBA1004505	75	R-HEMBA1004505	894
HEMBA1004785	F-HEMBA1004785	76	R-HEMBA1004785	895
HEMBA1004797	F-HEMBA1004797	77	R-HEMBA1004797	896
HEMBA1004952	F-HEMBA1004952	78	R-HEMBA1004952	897
HEMBA1004971	F-HEMBA1004971	79	R-HEMBA1004971	898
HEMBA1004982	F-HEMBA1004982	80	R-HEMBA1004982	899
HEMBA1005070	F-HEMBA1005070	81	R-HEMBA1005070	900
HEMBA1005084	F-HEMBA1005084	82	R-HEMBA1005084	901
HEMBA1005145	F-HEMBA1005145	83	R-HEMBA1005145	902
HEMBA1005230	F-HEMBA1005230	84	R-HEMBA1005230	903
HEMBA1005246	F-HEMBA1005246	85	R-HEMBA1005246	904
HEMBA1005267	F-HEMBA1005267	86	R-HEMBA1005267	905
HEMBA1005337	F-HEMBA1005337	87	R-HEMBA1005337	906
HEMBA1005430	F-HEMBA1005430	88	R-HEMBA1005430	907
HEMBA1005449	F-HEMBA1005449	89	R-HEMBA1005449	908
HEMBA1005489	F-HEMBA1005489	90	R-HEMBA1005489	909
HEMBA1005522	F-HEMBA1005522	91	R-HEMBA1005522	910
HEMBA1005545	F-HEMBA1005545	92	R-HEMBA1005545	911
HEMBA1005698	F-HEMBA1005698	93	R-HEMBA1005698	912
HEMBA1005913	F-HEMBA1005913	94	R-HEMBA1005913	913
HEMBA1005929	F-HEMBA1005929	95	R-HEMBA1005929	914

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
HEMBA1005945	F-HEMBA1005945	96	R-HEMBA1005945	915
HEMBA1006016	F-HEMBA1006016	97	R-HEMBA1006016	916
HEMBA1006171	F-HEMBA1006171	98	R-HEMBA1006171	917
HEMBA1006276	F-HEMBA1006276	99	R-HEMBA1006276	918
HEMBA1006299	F-HEMBA1006299	100	R-HEMBA1006299	919
HEMBA1006311	F-HEMBA1006311	101	R-HEMBA1006311	920
HEMBA1006335	F-HEMBA1006335	102	R-HEMBA1006335	921
HEMBA1006357	F-HEMBA1006357	103	R-HEMBA1006357	922
HEMBA1006430	F-HEMBA1006430	104	R-HEMBA1006430	923
HEMBA1006482	F-HEMBA1006482	105	R-HEMBA1006482	924
HEMBA1006517	F-HEMBA1006517	106	R-HEMBA1006517	925
HEMBA1006544	F-HEMBA1006544	107	R-HEMBA1006544	926
HEMBA1006572	F-HEMBA1006572	108	R-HEMBA1006572	927
HEMBA1006658	F-HEMBA1006658	109	R-HEMBA1006658	928
HEMBA1006707	F-HEMBA1006707	110	R-HEMBA1006707	929
HEMBA1006724	F-HEMBA1006724	111	R-HEMBA1006724	930
HEMBA1006749	F-HEMBA1006749	112	R-HEMBA1006749	931
HEMBA1006770	F-HEMBA1006770	113	R-HEMBA1006770	932
HEMBA1006902	F-HEMBA1006902	114	R-HEMBA1006902	933
HEMBA1006912	F-HEMBA1006912	115	R-HEMBA1006912	934
HEMBA1006916	F-HEMBA1006916	116	R-HEMBA1006916	935
HEMBA1006960	F-HEMBA1006960	117	R-HEMBA1006960	936
HEMBA1007013	F-HEMBA1007013	118	R-HEMBA1007013	937
HEMBA1007057	F-HEMBA1007057	119	R-HEMBA1007057	938
HEMBA1007063	F-HEMBA1007063	120	R-HEMBA1007063	939
HEMBA1007226	F-HEMBA1007226	121		
HEMBA1007241	F-HEMBA1007241	122	R-HEMBA1007241	940
HEMBA1007291	F-HEMBA1007291	123	R-HEMBA1007291	941
HEMBA1007332	F-HEMBA1007332	124	R-HEMBA1007332	942
HEMBB1000106	F-HEMBB1000106	125	R-HEMBB1000106	943
HEMBB1000276	F-HEMBB1000276	126	R-HEMBB1000276	944
HEMBB1000309	F-HEMBB1000309	127	R-HEMBB1000309	945
HEMBB1000407	F-HEMBB1000407	128	R-HEMBB1000407	946
HEMBB1000447	F-HEMBB1000447	129	R-HEMBB1000447	947
HEMBB1000542	F-HEMBB1000542	130	R-HEMBB1000542	948
HEMBB1000567	F-HEMBB1000567	131	R-HEMBB1000567	949
HEMBB1000642	F-HEMBB1000642	132	R-HEMBB1000642	950
HEMBB1000668	F-HEMBB1000668	133	R-HEMBB1000668	951
HEMBB1000679	F-HEMBB1000679	134	R-HEMBB1000679	952
HEMBB1000881	F-HEMBB1000881	135	R-HEMBB1000881	953
HEMBB1000905	F-HEMBB1000905	136	R-HEMBB1000905	954
HEMBB1001026	F-HEMBB1001026	137	R-HEMBB1001026	955
HEMBB1001048	F-HEMBB1001048	138	R-HEMBB1001048	956
HEMBB1001200	F-HEMBB1001200	139	R-HEMBB1001200	957
HEMBB1001407	F-HEMBB1001407	140	R-HEMBB1001407	958
HEMBB1001530	F-HEMBB1001530	141	R-HEMBB1001530	959
HEMBB1001547	F-HEMBB1001547	142	R-HEMBB1001547	960
HEMBB1001573	F-HEMBB1001573	143	R-HEMBB1001573	961

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
HEMBB1001847	F-HEMBB1001847	144	R-HEMBB1001847	962
HEMBB1001959	F-HEMBB1001959	145	R-HEMBB1001959	963
HEMBB1001978	F-HEMBB1001978	146	R-HEMBB1001978	964
HEMBB1002039	F-HEMBB1002039	147	R-HEMBB1002039	965
HEMBB1002041	F-HEMBB1002041	148	R-HEMBB1002041	966
HEMBB1002051	F-HEMBB1002051	149	R-HEMBB1002051	967
HEMBB1002120	F-HEMBB1002120	150	R-HEMBB1002120	968
HEMBB1002162	F-HEMBB1002162	151	R-HEMBB1002162	969
HEMBB1002228	F-HEMBB1002228	152	R-HEMBB1002228	970
HEMBB1002245	F-HEMBB1002245	153	R-HEMBB1002245	971
HEMBB1002302	F-HEMBB1002302	154	R-HEMBB1002302	972
HEMBB1002427	F-HEMBB1002427	155	R-HEMBB1002427	973
HEMBB1002465	F-HEMBB1002465	156	R-HEMBB1002465	974
HEMBB1002661	F-HEMBB1002661	157	R-HEMBB1002661	975
HEMBB1002663	F-HEMBB1002663	158	R-HEMBB1002663	976
HEMBB1002693	F-HEMBB1002693	159	R-HEMBB1002693	977
MAMMA 1000046	F-MAMMA1000046	160	R-MAMMA1000046	978
MAMMA1000102	F-MAMMA1000102	161	R-MAMMA1000102	979
MAMMA 1000106	F-MAMMA1000106	162	R-MAMMA1000106	980
MAMMA1000118	F-MAMMA1000118	163	R-MAMMA1000118	981
MAMMA1000141	F-MAMMA1000141	164	R-MAMMA1000141	982
MAMMA1000204	F-MAMMA1000204	165	R-MAMMA1000204	983
MAMMA1000226	F-MAMMA1000226	166	R-MAMMA1000226	984
MAMMA1000403	F-MAMMA1000403	167	R-MAMMA1000403	985
MAMMA1000449	F-MAMMA1000449	168	R-MAMMA1000449	986
MAMMA1000457	F-MAMMA1000457	169	R-MAMMA1000457	987
MAMMA1000473	F-MAMMA1000473	170	R-MAMMA1000473	988
MAMMA1000496	F-MAMMA1000496	171	R-MAMMA1000496	989
MAMMA1000528	F-MAMMA1000528	172	R-MAMMA1000528	990
MAMMA1000591	F-MAMMA1000591	173	R-MAMMA1000591	991
MAMMA 1000614	F-MAMMA1000614	174	R-MAMMA1000614	992
MAMMA1000652	F-MAMMA1000652	175	R-MAMMA1000652	993
MAMMA1000681	F-MAMMA1000681	176	R-MAMMA1000681	994
MAMMA 1000706	F-MAMMA1000706	177	R-MAMMA1000706	995
MAMMA 1000788	F-MAMMA1000788	178	R-MAMMA1000788	996
MAMMA 1000810	F-MAMMA1000810	179	R-MAMMA1000810	997
MAMMA1000814	F-MAMMA1000814	180	R-MAMMA1000814	998
MAMMA1000881	F-MAMMA1000881	181	R-MAMMA1000881	999
MAMMA1000986	F-MAMMA1000986	182	R-MAMMA1000986	1000
MAMMA 1000994	F-MAMMA1000994	183	R-MAMMA1000994	1001
MAMMA1001043	F-MAMMA1001043	184	R-MAMMA1001043	1002
MAMMA1001066	F-MAMMA1001066	185	R-MAMMA1001066	1003
MAMMA1001094	F-MAMMA1001094	186	R-MAMMA1001094	1004
MAMMA1001141	F-MAMMA1001141	187	R-MAMMA1001141	1005
MAMMA1001150	F-MAMMA1001150	188	R-MAMMA1001150	1006
MAMMA1001237	F-MAMMA1001237	189	R-MAMMA1001237	1007
MAMMA1001284	F-MAMMA1001284	190	R-MAMMA1001284	1008
MAMMA1001310	F-MAMMA1001310	191	R-MAMMA1001310	1009

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
MAMMA1001344	F-MAMMA1001344	192		
MAMMA1001418	F-MAMMA1001418	193	R-MAMMA1001418	1010
MAMMA1001532	F-MAMMA1001532	194	R-MAMMA1001532	1011
MAMMA1001609	F-MAMMA1001609	195	R-MAMMA1001609	1012
MAMMA 1001615	F-MAMMA1001615	196	R-MAMMA1001615	1013
MAMMA 1001623	F-MAMMA1001623	197	R-MAMMA1001623	1014
MAMMA1001634	F-MAMMA1001634	198	R-MAMMA1001634	1015
MAMMA 1001893	F-MAMMA1001893	199	R-MAMMA1001893	1016
MAMMA1001901	F-MAMMA1001901	200	R-MAMMA1001901	1017
MAMMA 1001957	F-MAMMA1001957	201	R-MAMMA1001957	1018
MAMMA1001978	F-MAMMA1001978	202	R-MAMMA1001978	1019
MAMMA1002070	F-MAMMA1002070	203	R-MAMMA1002070	1020
MAMMA1002080	F-MAMMA1002080	204	R-MAMMA1002080	1021
MAMMA 1002087	F-MAMMA1002087	205	R-MAMMA1002087	1022
MAMMA1002091	F-MAMMA1002091	206		
MAMMA 1002095	F-MAMMA1002095	207	R-MAMMA1002095	1023
MAMMA 1002128	F-MAMMA1002128	208	R-MAMMA1002128	1024
MAMMA1002142	F-MAMMA1002142	209	R-MAMMA1002142	1025
MAMMA1002165	F-MAMMA1002165	210	R-MAMMA1002165	1026
MAMMA 1002205	F-MAMMA1002205	211	R-MAMMA1002205	1027
MAMMA 1002224	F-MAMMA1002224	212	R-MAMMA1002224	1028
MAMMA1002234	F-MAMMA1002234	213	R-MAMMA1002234	1029
MAMMA1002586	F-MAMMA1002586	214	R-MAMMA1002586	1030
MAMMA1002633	F-MAMMA1002633	215	R-MAMMA1002633	1031
MAMMA1003126	F-MAMMA1003126	216	R-MAMMA1003126	1032
NT2RM1000407	F-NT2RM1000407	217		
NT2RM1000462	F-NT2RM1000462	218		
NT2RM1000542	F-NT2RM1000542	219		
NT2RM1000580	F-NT2RM1000580	220		
NT2RM1000789	F-NT2RM1000789	221		
NT2RM1000855	F-NT2RM1000855	222		
NT2RM1000858	F-NT2RM1000858	223		
NT2RM1000899	F-NT2RM1000899	224		
NT2RM2000241	F-NT2RM2000241	225		
NT2RM2000306	F-NT2RM2000306	226		
NT2RM2000410	F-NT2RM2000410	227		
NT2RM2000423	F-NT2RM2000423	228		
NT2RM2000497	F-NT2RM2000497	229		
NT2RM2000514	F-NT2RM2000514	230		
NT2RM2000565	F-NT2RM2000565	231		
NT2RM2000582	F-NT2RM2000582	232		
NT2RM2000589	F-NT2RM2000589	233		
NT2RM2000622	F-NT2RM2000622	234		
NT2RM2000632	F-NT2RM2000632	235		
NT2RM2000773	F-NT2RM2000773	236		
NT2RM2001126	F-NT2RM2001126	237		
NT2RM2001558	F-NT2RM2001558	238		
NT2RM2001626	F-NT2RM2001626	239		

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
NT2RM2001643	F-NT2RM2001643	240		
NT2RM2001738	F-NT2RM2001738	241		
NT2RM2001767	F-NT2RM2001767	242		
NT2RM2001792	F-NT2RM2001792	243		
NT2RM2001818	F-NT2RM2001818	244		
NT2RM2001902	F-NT2RM2001902	245		
NT2RM2001939	F-NT2RM2001939	246		
NT2RM2001941	F-NT2RM2001941	247		
NT2RM4000100	F-NT2RM4000100	248	R-NT2RM4000100	1033
NT2RM4000115	F-NT2RM4000115	249	R-NT2RM4000115	1034
NT2RM4000198	F-NT2RM4000198	250	R-NT2RM4000198	1035
NT2RM4000284	F-NT2RM4000284	251	R-NT2RM4000284	1036
NT2RM4000295	F-NT2RM4000295	252	R-NT2RM4000295	1037
NT2RM4000326	F-NT2RM4000326	253	R-NT2RM4000326	1038
NT2RM4000417	F-NT2RM4000417	254	R-NT2RM4000417	1039
NT2RM4000444	F-NT2RM4000444	255	R-NT2RM4000444	1040
NT2RM4000587	F-NT2RM4000587	256	R-NT2RM4000587	1041
NT2RM4000593	F-NT2RM4000593	257	R-NT2RM4000593	1042
NT2RM4000648	F-NT2RM4000648	258	R-NT2RM4000648	1043
NT2RM4000761	F-NT2RM4000761	259	R-NT2RM4000761	1044
NT2RM4000965	F-NT2RM4000965	260	R-NT2RM4000965	1045
NT2RM4000997	F-NT2RM4000997	261	R-NT2RM4000997	1046
NT2RM4001321	F-NT2RM4001321	262	R-NT2RM4001321	1047
NT2RM4001325	F-NT2RM4001325	263	R-NT2RM4001325	1048
NT2RM4001377	F-NT2RM4001377	264	R-NT2RM4001377	1049
NT2RM4001735	F-NT2RM4001735	265	R-NT2RM4001735	1050
NT2RM4001768	F-NT2RM4001768	266	R-NT2RM4001768	1051
NT2RM4001843	F-NT2RM4001843	267	R-NT2RM4001843	1052
NT2RM4002352	F-NT2RM4002352	268	R-NT2RM4002352	1053
NT2RP1000002	F-NT2RP1000002	269		
NT2RP1000050	F-NT2RP1000050	270		
NT2RP1000181	F-NT2RP1000181	271		
NT2RP1000239	F-NT2RP1000239	272		
NT2RP1000261	F-NT2RP1000261	273		
NT2RP1000271	F-NT2RP1000271	274		
NT2RP1000300	F-NT2RP1000300	275		
NT2RP1000325	F-NT2RP1000325	276		
NT2RP1000448	F-NT2RP1000448	277		
NT2RP1000465	F-NT2RP1000465	278		
NT2RP1000468	F-NT2RP1000468	279		
NT2RP1000551	F-NT2RP1000551	280		
NT2RP1000579	F-NT2RP1000579	281		
NT2RP1000613	F-NT2RP1000613	282		
NT2RP1000679	F-NT2RP1000679	283		
NT2RP1000740	F-NT2RP1000740	284		
NT2RP1000903	F-NT2RP1000903	285		
NT2RP1000981	F-NT2RP1000981	286		
NT2RP1001004	F-NT2RP1001004	287		

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
NT2RP1001020	F-NT2RP1001020	288		
NT2RP1001031	F-NT2RP1001031	289		
NT2RP1001563	F-NT2RP1001563	290		
NT2RP2000092	F-NT2RP2000092	291	R-NT2RP2000092	1054
NT2RP2000178	F-NT2RP2000178	292	R-NT2RP2000178	1055
NT2RP2000240	F-NT2RP2000240	293	R-NT2RP2000240	1056
NT2RP2000394	F-NT2RP2000394	294	R-NT2RP2000394	1057
NT2RP2000447	F-NT2RP2000447	295	R-NT2RP2000447	1058
NT2RP2000479	F-NT2RP2000479	296	R-NT2RP2000479	1059
NT2RP2000514	F-NT2RP2000514	297	R-NT2RP2000514	1060
NT2RP2000533	F-NT2RP2000533	298	R-NT2RP2000533	1061
NT2RP2000610	F-NT2RP2000610	299		
NT2RP2000616	F-NT2RP2000616	300	R-NT2RP2000616	1062
NT2RP2000649	F-NT2RP2000649	301	R-NT2RP2000649	1063
NT2RP2000663	F-NT2RP2000663	302	R-NT2RP2000663	1064
NT2RP2000694	F-NT2RP2000694	303		
NT2RP2000712	F-NT2RP2000712	304	R-NT2RP2000712	1065
NT2RP2000739	F-NT2RP2000739	305	R-NT2RP2000739	1066
NT2RP2000818	F-NT2RP2000818	306	R-NT2RP2000818	1067
NT2RP2000903	F-NT2RP2000903	307	R-NT2RP2000903	1068
NT2RP2001200	F-NT2RP2001200	308	R-NT2RP2001200	1069
NT2RP2001223	F-NT2RP2001223	309	R-NT2RP2001223	1070
NT2RP2001276	F-NT2RP2001276	310	R-NT2RP2001276	1071
NT2RP2001388	F-NT2RP2001388	311	R-NT2RP2001388	1072
NT2RP2001469	F-NT2RP2001469	312	R-NT2RP2001469	1073
NT2RP2001480	F-NT2RP2001480	313	R-NT2RP2001480	1074
NT2RP2001495	F-NT2RP2001495	314	R-NT2RP2001495	1075
NT2RP2001514	F-NT2RP2001514	315	R-NT2RP2001514	1076
NT2RP2001529	F-NT2RP2001529	316		
NT2RP2001538	F-NT2RP2001538	317	R-NT2RP2001538	1077
NT2RP2001562	F-NT2RP2001562	318	R-NT2RP2001562	1078
NT2RP2001662	F-NT2RP2001662	319	R-NT2RP2001662	1079
NT2RP2001755	F-NT2RP2001755	320	R-NT2RP2001755	1080
NT2RP2001769	F-NT2RP2001769	321	R-NT2RP2001769	1081
NT2RP2001817	F-NT2RP2001817	322	R-NT2RP2001817	1082
NT2RP2001878	F-NT2RP2001878	323	R-NT2RP2001878	1083
NT2RP2001903	F-NT2RP2001903	324	R-NT2RP2001903	1084
NT2RP2001915	F-NT2RP2001915	325	R-NT2RP2001915	1085
NT2RP2001921	F-NT2RP2001921	326	R-NT2RP2001921	1086
NT2RP2001948	F-NT2RP2001948	327	R-NT2RP2001948	1087
NT2RP2001956	F-NT2RP2001956	328	R-NT2RP2001956	1088
NT2RP2002015	F-NT2RP2002015	329	R-NT2RP2002015	1089
NT2RP2002063	F-NT2RP2002063	330	R-NT2RP2002063	1090
NT2RP2002188	F-NT2RP2002188	331	R-NT2RP2002188	1091
NT2RP2002232	F-NT2RP2002232	332	R-NT2RP2002232	1092
NT2RP2002304	F-NT2RP2002304	333	R-nnnnnnnnnnn	1093
NT2RP2002409	F-NT2RP2002409	334	R-NT2RP2002409	1094
NT2RP2002510	F-NT2RP2002510	335	R-NT2RP2002510	1095

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
NT2RP2002527	F-NT2RP2002527	336	R-NT2RP2002527	1096
NT2RP2002533	F-NT2RP2002533	337	R-NT2RP2002533	1097
NT2RP2002564	F-NT2RP2002564	338	R-NT2RP2002564	1098
NT2RP2002674	F-NT2RP2002674	339	R-NT2RP2002674	1099
NT2RP2002721	F-NT2RP2002721	340	R-NT2RP2002721	1100
NT2RP2002824	F-NT2RP2002824	341	R-NT2RP2002824	1101
NT2RP2002942	F-NT2RP2002942	342	R-NT2RP2002942	1102
NT2RP2002974	F-NT2RP2002974	343	R-NT2RP2002974	1103
NT2RP2002976	F-NT2RP2002976	344	R-NT2RP2002976	1104
NT2RP2003042	F-NT2RP2003042	345	R-NT2RP2003042	1105
NT2RP2003138	F-NT2RP2003138	346		
NT2RP2003179	F-NT2RP2003179	347	R-NT2RP2003179	1106
NT2RP2003210	F-NT2RP2003210	348	R-NT2RP2003210	1107
NT2RP2003302	F-NT2RP2003302	349	R-NT2RP2003302	1108
NT2RP2003369	F-NT2RP2003369	350	R-NT2RP2003369	1109
NT2RP2003383	F-NT2RP2003383	351	R-NT2RP2003383	1110
NT2RP2003390	F-NT2RP2003390	352	R-NT2RP2003390	1111
NT2RP2003469	F-NT2RP2003469	353	R-NT2RP2003469	1112
NT2RP2003545	F-NT2RP2003545	354	R-NT2RP2003545	1113
NT2RP2003593	F-NT2RP2003593	355	R-NT2RP2003593	1114
NT2RP2003599	F-NT2RP2003599	356	R-NT2RP2003599	1115
NT2RP2003655	F-NT2RP2003655	357	R-NT2RP2003655	1116
NT2RP2003664	F-NT2RP2003664	358	R-NT2RP2003664	1117
NT2RP2003931	F-NT2RP2003931	359	R-NT2RP2003931	1118
NT2RP2003940	F-NT2RP2003940	360	R-NT2RP2003940	1119
NT2RP2003950	F-NT2RP2003950	361	R-NT2RP2003950	1120
NT2RP2004069	F-NT2RP2004069	362	R-NT2RP2004069	1121
NT2RP2004108	F-NT2RP2004108	363	R-NT2RP2004108	1122
NT2RP2004141	F-NT2RP2004141	364	R-NT2RP2004141	1123
NT2RP2004179	F-NT2RP2004179	365	R-NT2RP2004179	1124
NT2RP2004205	F-NT2RP2004205	366	R-NT2RP2004205	1125
NT2RP2004447	F-NT2RP2004447	367	R-NT2RP2004447	1126
NT2RP2004495	F-NT2RP2004495	368	R-NT2RP2004495	1127
NT2RP2004524	F-NT2RP2004524	369	R-NT2RP2004524	1128
NT2RP2004556	F-NT2RP2004556	370	R-NT2RP2004556	1129
NT2RP2004606	F-NT2RP2004606	371	R-NT2RP2004606	1130
NT2RP2004648	F-NT2RP2004648	372	R-NT2RP2004648	1131
NT2RP2004670	F-NT2RP200467()	373	R-NT2RP2004670	1132
NT2RP2004794	F-NT2RP2004794	374	R-NT2RP2004794	1133
NT2RP2004837	F-NT2RP2004837	375	R-NT2RP2004837	1134
NT2RP2004847	F-NT2RP2004847	376	R-NT2RP2004847	1135
NT2RP2005027	F-NT2RP2005027	377	R-NT2RP2005027	1136
NT2RP2005069	F-NT2RP2005069	378	R-NT2RP2005069	1137
NT2RP2005163	F-NT2RP2005163	379	R-NT2RP2005163	1138
NT2RP2005181	F-NT2RP2005181	380	R-NT2RP2005181	1139
NT2RP2005247	F-NT2RP2005247	381	R-NT2RP2005247	1140
NT2RP2005378	F-NT2RP2005378	382	R-NT2RP2005378	1141
NT2RP2005391	F-NT2RP2005391	383	R-NT2RP2005391	1142

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
NT2RP2005425	F-NT2RP2005425	384	R-NT2RP2005425	1143
NT2RP2005463	F-NT2RP2005463	385	R-NT2RP2005463	1144
NT2RP2005514	F-NT2RP2005514	386	R-NT2RP2005514	1145
NT2RP2005535	F-NT2RP2005535	387	R-NT2RP2005535	1146
NT2RP2005541	F-NT2RP2005541	388	R-NT2RP2005541	1147
NT2RP2005597	F-NT2RP2005597	389	R-NT2RP2005597	1148
NT2RP2005632	F-NT2RP2005632	390	R-nnnnnnnnnnn	1149
NT2RP2005666	F-NT2RP2005666	391	R-NT2RP2005666	1150
NT2RP2005774	F-NT2RP2005774	392	R-NT2RP2005774	1151
NT2RP2005878	F-NT2RP2005878	393	R-NT2RP2005878	1152
NT2RP2005883	F-NT2RP2005883	394	R-NT2RP2005883	1153
NT2RP2005887	F-NT2RP2005887	395	R-NT2RP2005887	1154
NT2RP2005941	F-NT2RP2005941	396	R-nnnnnnnnnnn	1155
NT2RP2005994	F-NT2RP2005994	397	R-NT2RP2005994	1156
NT2RP2006004	F-NT2RP2006004	398	R-NT2RP2006004	1157
NT2RP2006042	F-NT2RP2006042	399	R-NT2RP2006042	1158
NT2RP2006092	F-NT2RP2006092	400	R-NT2RP2006092	1159
NT2RP2006099	F-NT2RP2006099	401	R-NT2RP2006099	1160
NT2RP2006134	F-NT2RP2006134	402	R-NT2RP2006134	1161
NT2RP2006269	F-NT2RP2006269	403	R-NT2RP2006269	1162
NT2RP2006512	F-NT2RP2006512	404	R-NT2RP2006512	1163
NT2RP3000011	F-NT2RP3000011	405	R-NT2RP3000011	1164
NT2RP3000022	F-NT2RP3000022	406	R-NT2RP3000022	1165
NT2RP3000059	F-NT2RP3000059	407	R-NT2RP3000059	1166
NT2RP3000063	F-NT2RP3000063	408	R-NT2RP3000063	1167
NT2RP3000125	F-NT2RP3000125	409	R-nnnnnnnnnnn	1168
NT2RP3000148	F-NT2RP3000148	410	R-NT2RP3000148	1169
NT2RP3000169	F-NT2RP3000169	411	R-NT2RP3000169	1170
NT2RP3000171	F-NT2RP3000171	412	R-NT2RP3000171	1171
NT2RP3000172	F-NT2RP3000172	413	R-NT2RP3000172	1172
NT2RP3000201	F-NT2RP3000201	414	R-NT2RP3000201	1173
NT2RP3000232	F-NT2RP3000232	415	R-NT2RP3000232	1174
NT2RP3000304	F-NT2RP3000304	416	R-NT2RP3000304	1175
NT2RP3000378	F-NT2RP3000378	417	R-NT2RP3000378	1176
NT2RP3000427	F-NT2RP3000427	418		
NT2RP3000436	F-NT2RP3000436	419	R-NT2RP3000436	1177
NT2RP3000444	F-NT2RP3000444	420	R-NT2RP3000444	1178
NT2RP3000460	F-NT2RP3000460	421	R-NT2RP3000460	1179
NT2RP3000481	F-NT2RP3000481	422	R-NT2RP3000481	1180
NT2RP3000616	F-NT2RP3000616	423	R-NT2RP3000616	1181
NT2RP3000645	F-NT2RP3000645	424	R-NT2RP3000645	1182
NT2RP3000652	F-NT2RP3000652	425	R-NT2RP3000652	1183
NT2RP3000676	F-NT2RP3000676	426	R-NT2RP3000676	1184
NT2RP3000677	F-NT2RP3000677	427	R-NT2RP3000677	1185
NT2RP3000721	F-NT2RP3000721	428	R-NT2RP3000721	1186
NT2RP3000789	F-NT2RP3000789	429	R-NT2RP3000789	1187
NT2RP3000818	F-NT2RP3000818	430	R-NT2RP3000818	1188
NT2RP3000820	F-NT2RP3000820	431	R-NT2RP3000820	1189

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
NT2RP3000838	F-NT2RP3000838	432	R-NT2RP3000838	1190
NT2RP3000871	F-NT2RP3000871	433	R-NT2RP3000871	1191
NT2RP3000907	F-NT2RP3000907	434	R-NT2RP3000907	1192
NT2RP3000921	F-NT2RP3000921	435	R-NT2RP3000921	1193
NT2RP3001012	F-NT2RP3001012	436	R-NT2RP3001012	1194
NT2RP3001044	F-NT2RP3001044	437	R-NT2RP3001044	1195
NT2RP3001061	F-NT2RP3001061	438	R-NT2RP3001061	1196
NT2RP3001159	F-NT2RP3001159	439	R-NT2RP3001159	1197
NT2RP3001170	F-NT2RP3001170	440	R-NT2RP3001170	1198
NT2RP3001195	F-NT2RP3001195	441	R-NT2RP3001195	1199
NT2RP3001240	F-NT2RP3001240	442	R-NT2RP3001240	1200
NT2RP3001271	F-NT2RP3001271	443	R-NT2RP3001271	1201
NT2RP3001322	F-NT2RP3001322	444	R-NT2RP3001322	1202
NT2RP3001388	F-NT2RP3001388	445		
NT2RP3001542	F-NT2RP3001542	446	R-NT2RP3001542	1203
NT2RP3001560	F-NT2RP3001560	447	R-NT2RP3001560	1204
NT2RP3001592	F-NT2RP3001592	448	R-NT2RP3001592	1205
NT2RP3001650	F-NT2RP3001650	449		
NT2RP3001685	F-NT2RP3001685	450	R-NT2RP3001685	1206
NT2RP3001738	F-NT2RP3001738	451	R-NT2RP3001738	1207
NT2RP3001754	F-NT2RP3001754	452	R-NT2RP3001754	1208
NT2RP3001858	F-NT2RP3001858	453	R-NT2RP3001858	1209
NT2RP3001976	F-NT2RP3001976	454	R-NT2RP3001976	1210
NT2RP3002015	F-NT2RP3002015	455	R-NT2RP3002015	1211
NT2RP3002160	F-NT2RP3002160	456	R-NT2RP3002160	1212
NT2RP3002281	F-NT2RP3002281	457	R-NT2RP3002281	1213
NT2RP3002286	F-NT2RP3002286	458	R-NT2RP3002286	1214
NT2RP3002311	F-NT2RP3002311	459	R-NT2RP3002311	1215
NT2RP3002324	F-NT2RP3002324	460	R-NT2RP3002324	1216
NT2RP3002342	F-NT2RP3002342	461	R-NT2RP3002342	1217
NT2RP3002353	F-NT2RP3002353	462	R-NT2RP3002353	1218
NT2RP3002409	F-NT2RP3002409	463	R-NT2RP3002409	1219
NT2RP3002411	F-NT2RP3002411	464	R-NT2RP3002411	1220
NT2RP3002448	F-NT2RP3002448	465	R-NT2RP3002448	1221
NT2RP3002571	F-NT2RP3002571	466	R-NT2RP3002571	1222
NT2RP3002664	F-NT2RP3002664	467	R-NT2RP3002664	1223
NT2RP3002721	F-NT2RP3002721	468	R-NT2RP3002721	1224
NT2RP3002737	F-NT2RP3002737	469	R-NT2RP3002737	1225
NT2RP3002738	F-NT2RP3002738	470	R-NT2RP3002738	1226
NT2RP3002790	F-NT2RP3002790	471	R-NT2RP3002790	1227
NT2RP3002836	F-NT2RP3002836	472	R-NT2RP3002836	1228
NT2RP3002887	F-NT2RP3002887	473	R-NT2RP3002887	1229
NT2RP3002900	F-NT2RP3002900	474	R-NT2RP3002900	1230
NT2RP3002958	F-NT2RP3002958	475	R-NT2RP3002958	1231
NT2RP3002983	F-NT2RP3002983	476	R-NT2RP3002983	1232
NT2RP3003000	F-NT2RP3003000	477	R-NT2RP3003000	1233
NT2RP3003076	F-NT2RP3003076	478	R-NT2RP3003076	1234
NT2RP3003354	F-NT2RP3003354	479	R-NT2RP3003354	1235

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
NT2RP3003448	F-NT2RP3003448	480	R-NT2RP3003448	1236
NT2RP3003469	F-NT2RP3003469	481	R-NT2RP3003469	1237
NT2RP3003473	F-NT2RP3003473	482	R-NT2RP3003473	1238
NT2RP3003527	F-NT2RP3003527	483	R-NT2RP3003527	1239
NT2RP3003532	F-NT2RP3003532	484	R-NT2RP3003532	1240
NT2RP3003535	F-NT2RP3003535	485	R-nnnnnnnnnnn	1241
NT2RP3003559	F-NT2RP3003559	486	R-NT2RP3003559	1242
NT2RP3003614	F-NT2RP3003614	487	R-NT2RP3003614	1243
NT2RP3003729	F-NT2RP3003729	488	R-NT2RP3003729	1244
NT2RP3003849	F-NT2RP3003849	489	R-NT2RP3003849	1245
NT2RP3003874	F-NT2RP3003874	490	R-NT2RP3003874	1246
NT2RP3003939	F-NT2RP3003939	491		
NT2RP3003963	F-NT2RP3003963	492	R-NT2RP3003963	1247
NT2RP3004000	F-NT2RP3004000	493	R-NT2RP3004000	1248
NT2RP3004025	F-NT2RP3004025	494	R-NT2RP3004025	1249
NT2RP3004067	F-NT2RP3004067	495		
NT2RP3004075	F-NT2RP3004075	496	R-NT2RP3004075	1250
NT2RP3004083	F-NT2RP3004083	497	R-NT2RP3004083	1251
NT2RP3004090	F-NT2RP3004090	498	R-NT2RP3004090	1252
NT2RP3004119	F-NT2RP3004119	499	R-NT2RP3004119	1253
NT2RP3004130	F-NT2RP3004130	500	R-NT2RP3004130	1254
NT2RP3004133	F-NT2RP3004133	501	R-NT2RP3004133	1255
NT2RP3004202	F-NT2RP3004202	502	R-NT2RP3004202	1256
NT2RP3004294	F-NT2RP3004294	503	R-NT2RP3004294	1257
NT2RP3004309	F-NT2RP3004309	504	R-NT2RP3004309	1258
NT2RP3004321	F-NT2RP3004321	505	R-NT2RP3004321	1259
NT2RP3004345	F-NT2RP3004345	506	R-NT2RP3004345	1260
NT2RP3004355	F-NT2RP3004355	507	R-NT2RP3004355	1261
NT2RP3004374	F-NT2RP3004374	508	R-NT2RP3004374	1262
NT2RP3004406	F-NT2RP3004406	509	R-NT2RP3004406	1263
NT2RP3004481	F-NT2RP3004481	510	R-NT2RP3004481	1264
NT2RP3004552	F-NT2RP3004552	511	R-NT2RP3004552	1265
NT2RP3004557	F-NT2RP3004557	512		
NT2RP3004625	F-NT2RP3004625	513	R-NT2RP3004625	1266
NT2RP3004640	F-NT2RP3004640	514	R-NT2RP3004640	1267
NT2RP3004647	F-NT2RP3004647	515	R-NT2RP3004647	1268
NT2RP4000108	F-NT2RP4000108	516	R-NT2RP4000108	1269
NT2RP4000634	F-NT2RP4000634	517	R-NT2RP4000634	1270
NT2RP4000962	F-NT2RP4000962	518	R-NT2RP4000962	1271
NT2RP4001001	F-NT2RP4001001	519	R-NT2RP4001001	1272
NT2RP4001009	F-NT2RP4001009	520	R-NT2RP4001009	1273
NT2RP4001467	F-NT2RP4001467	521	R-NT2RP4001467	1274
NT2RP4001877	F-NT2RP4001877	522	R-NT2RP4001877	1275
NT2RP4001879	F-NT2RP4001879	523	R-NT2RP4001879	1276
NT2RP4002187	F-NT2RP4002187	524	R-NT2RP4002187	1277
NT2RP4002451	F-NT2RP4002451	525	R-NT2RP4002451	1278
NT2RP4002715	F-NT2RP4002715	526	R-NT2RP4002715	1279
NT2RP4002750	F-NT2RP4002750	527	R-NT2RP4002750	1280

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
OVARC1000003	F-OVARC1000003	528	R-OVARC1000003	1281
OVARC1000090	F-OVARC1000090	529	R-OVARC1000090	1282
OVARC1000105	F-OVARC1000105	530	R-OVARC1000105	1283
OVARC1000137	F-OVARC1000137	531	R-OVARC1000137	1284
OVARC1000208	F-OVARC1000208	532	R-OVARC1000208	1285
OVARC1000255	F-OVARC1000255	533	R-OVARC1000255	1286
OVARC1000275	F-OVARC1000275	534	R-OVARC1000275	1287
OVARC1000298	F-OVARC1000298	535	R-OVARC1000298	1288
OVARC1000307	F-OVARC1000307	536	R-OVARC1000307	1289
OVARC1000313	F-OVARC1000313	537	R-OVARC1000313	1290
OVARC1000331	F-OVARC1000331	538	R-OVARC1000331	1291
OVARC1000410	F-OVARC1000410	539	R-OVARC1000410	1292
OVARC1000439	F-OVARC1000439	540	R-OVARC1000439	1293
OVARC1000467	F-OVARC1000467	541	R-OVARC1000467	1294
OVARC1000529	F-OVARC1000529	542	R-OVARC1000529	1295
OVARC1000553	F-OVARC1000553	543	R-OVARC1000553	1296
OVARC1000775	F-OVARC1000775	544	R-OVARC1000775	1297
OVARC1000811	F-OVARC1000811	545	R-OVARC1000811	1298
OVARC1000853	F-OVARC1000853	546	R-OVARC1000853	1299
OVARC1000873	F-OVARC1000873	547	R-OVARC1000873	1300
OVARC1000916	F-OVARC1000916	548	R-OVARC1000916	1301
OVARC1000956	F-OVARC1000956	549	R-OVARC1000956	1302
OVARC1000995	F-OVARC1000995	550	R-OVARC1000995	1303
OVARC1001030	F-OVARC1001030	551	R-OVARC1001030	1304
OVARC1001049	F-OVARC1001049	552	R-OVARC1001049	1305
OVARC1001086	F-OVARC1001086	553	R-OVARC1001086	1306
OVARC1001132	F-OVARC1001132	554	R-OVARC1001132	1307
OVARC1001163	F-OVARC1001163	555	R-OVARC1001163	1308
OVARC1001222	F-OVARC1001222	556	R-OVARC1001222	1309
OVARC1001260	F-OVARC1001260	557	R-OVARC1001260	1310
OVARC1001336	F-OVARC1001336	558	R-OVARC1001336	1311
OVARC1001338	F-OVARC1001338	559	R-OVARC1001338	1312
OVARC1001569	F-OVARC1001569	560	R-OVARC1001569	1313
OVARC1001570	F-OVARC1001570	561	R-OVARC1001570	1314
OVARC1001596	F-OVARC1001596	562	R-OVARC1001596	1315
OVARC1001607	F-OVARC1001607	563	R-OVARC1001607	1316
OVARC1001725	F-OVARC1001725	564	R-OVARC1001725	1317
OVARC1001727	F-OVARC1001727	565	R-OVARC1001727	1318
OVARC1001807	F-OVARC1001807	566	R-OVARC1001807	1319
OVARC1001833	F-OVARC1001833	567	R-OVARC1001833	1320
OVARC1001952	F-OVARC1001952	568		
OVARC1001991	F-OVARC1001991	569	R-OVARC1001991	1321
OVARC1002058	F-OVARC1002058	570	R-OVARC1002058	1322
OVARC1002178	F-OVARC1002178	571	R-OVARC1002178	1323
PLACE 1000033	F-PLACE1000033	572	R-PLACE1000033	1324
PLACE 1000231	F-PLACE1000231	573	R-PLACE1000231	1325
PLACE 1000258	F-PLACE1000258	574	R-PLACE1000258	1326
PLACE 1000442	F-PLACE1000442	575	R-PLACE1000442	1327

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
PLACE 1000560	F-PLACE1000560	576	R-PLACE1000560	1328
PLACE 1000740	F-PLACE1000740	577	R-PLACE1000740	1329
PLACE 1000907	F-PLACE1000907	578		
PLACE 1000912	F-PLACE1000912	579	R-PLACE1000912	1330
PLACE 1000914	F-PLACE1000914	580	R-PLACE1000914	1331
PLACE 1000927	F-PLACE1000927	581	R-PLACE1000927	1332
PLACE 1000986	F-PLACE1000986	582	R-PLACE1000986	1333
PLACE1001016	F-PLACE1001016	583	R-PLACE1001016	1334
PLACE 1001100	F-PLACE1001100	584	R-PLACE1001100	1335
PLACE 1001114	F-PLACE1001114	585	R-PLACE1001114	1336
PLACE 1001123	F-PLACE1001123	586	R-PLACE1001123	1337
PLACE 1001183	F-PLACE1001183	587	R-PLACE1001183	1338
PLACE 1001229	F-PLACE1001229	588	R-PLACE1001229	1339
PLACE 1001231	F-PLACE1001231	589	R-PLACE1001231	1340
PLACE 1001340	F-PLACE1001340	590	R-PLACE1001340	1341
PLACE1001401	F-PLACE1001401	591	R-PLACE1001401	1342
PLACE 1001407	F-PLACE1001407	592	R-PLACE1001407	1343
PLACE 1001464	F-PLACE1001464	593	R-PLACE1001464	1344
PLACE1001500	F-PLACE1001500	594	R-PLACE1001500	1345
PLACE1001516	F-PLACE1001516	595	R-PLACE1001516	1346
PLACE1001536	F-PLACE1001536	596	R-PLACE1001536	1347
PLACE 1001564	F-PLACE1001564	597	R-PLACE1001564	1348
PLACE 1001655	F-PLACE1001655	598	R-PLACE1001655	1349
PLACE 1001788	F-PLACE1001788	599	R-PLACE1001788	1350
PLACE1001795	F-PLACE1001795	600	R-PLACE1001795	1351
PLACE1001836	F-PLACE1001836	601	R-PLACE1001836	1352
PLACE 1001918	F-PLACE1001918	602	R-PLACE1001918	1353
PLACE 1001949	F-PLACE1001949	603	R-PLACE1001949	1354
PLACE 1002080	F-PLACE1002080	604	R-PLACE1002080	1355
PLACE 1002095	F-PLACE1002095	605	R-PLACE1002095	1356
PLACE 1002153	F-PLACE1002153	606	R-PLACE1002153	1357
PLACE 1002329	F-PLACE1002329	607	R-PLACE1002329	1358
PLACE 1002355	F-PLACE1002355	608	R-PLACE1002355	1359
PLACE1002374	F-PLACE1002374	609	R-PLACE1002374	1360
PLACE 1002518	F-PLACE1002518	610	R-PLACE1002518	1361
PLACE 1002547	F-PLACE1002547	611	R-PLACE1002547	1362
PLACE 1002726	F-PLACE1002726	612	R-PLACE1002726	1363
PLACE 1002905	F-PLACE1002905	613	R-PLACE1002905	1364
PLACE 1002911	F-PLACE1002911	614	R-PLACE1002911	1365
PLACE 1002967	F-PLACE1002967	615	R-PLACE1002967	1366
PLACE 1003135	F-PLACE1003135	616	R-PLACE1003135	1367
PLACE1003163	F-PLACE1003163	617	R-PLACE1003163	1368
PLACE 1003407	F-PLACE1003407	618	R-PLACE1003407	1369
PLACE 1003428	F-PLACE1003428	619	R-PLACE1003428	1370
PLACE1003438	F-PLACE1003438	620	R-PLACE1003438	1371
PLACE 1003460	F-PLACE1003460	621	R-PLACE1003460	1372
PLACE 1003529	F-PLACE1003529	622	R-nnnnnnnnnnnn	1373
PLACE 1003573	F-PLACE1003573	623	R-PLACE1003573	1374

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
PLACE 1003598	F-PLACE1003598	624	R-PLACE1003598	1375
PLACE1003644	F-PLACE1003644	625	R-PLACE1003644	1376
PLACE1003737	F-PLACE1003737	626	R-PLACE1003737	1377
PLACE 1003772	F-PLACE1003772	627	R-PLACE1003772	1378
PLACE 1003839	F-PLACE1003839	628	R-PLACE1003839	1379
PLACE 1003845	F-PLACE1003845	629	R-PLACE1003845	1380
PLACE 1003 852	F-PLACE1003852	630	R-PLACE1003852	1381
PLACE 1004028	F-PLACE1004028	631	R-PLACE1004028	1382
PLACE 1004078	F-PLACE1004078	632	R-PLACE1004078	1383
PLACE1004166	F-PLACE1004166	633	R-PLACE1004166	1384
PLACE 1004168	F-PLACE1004168	634	R-nnnnnnnnnnnn	1385
PLACE1004199	F-PLACE1004199	635	R-PLACE1004199	1386
PLACE 1004279	F-PLACE1004279	636	R-PLACE1004279	1387
PLACE 1004282	F-PLACE1004282	637	R-PLACE1004282	1388
PLACE 1004305	F-PLACE1004305	638	R-PLACE1004305	1389
PLACE 1004441	F-PLACE1004441	639	R-PLACE1004441	1390
PLACE 1004450	F-PLACE1004450	640	R-PLACE1004450	1391
PLACE 1004482	F-PLACE1004482	641	R-PLACE1004482	1392
PLACE 1004492	F-PLACE1004492	642	R-PLACE1004492	1393
PLACE 1004519	F-PLACE1004519	643	R-PLACE1004519	1394
PLACE 1004520	F-PLACE1004520	644	R-PLACE1004520	1395
PLACE 1004630	F-PLACE1004630	645	R-PLACE1004630	1396
PLACE 1004637	F-PLACE1004637	646	R-PLACE1004637	1397
PLACE 1004648	F-PLACE1004648	647	R-PLACE1004648	1398
PLACE 1004816	F-PLACE1004816	648	R-PLACE1004816	1399
PLACE 1004887	F-PLACE1004887	649	R-PLACE1004887	1400
PLACE 1005003	F-PLACE1005003	650	R-PLACE1005003	1401
PLACE 1005005	F-PLACE1005005	651	R-PLACE1005005	1402
PLACE 1005031	F-PLACE1005031	652	R-PLACE1005031	1403
PLACE 1005239	F-PLACE1005239	653	R-PLACE1005239	1404
PLACE 1005250	F-PLACE1005250	654	R-PLACE1005250	1405
PLACE 1005383	F-PLACE1005383	655	R-PLACE1005383	1406
PLACE 1005410	F-PLACE1005410	656	R-PLACE1005410	1407
PLACE 1005426	F-PLACE1005426	657	R-PLACE1005426	1408
PLACE 1005519	F-PLACE1005519	658	R-PLACE1005519	1409
PLACE 1005539	F-PLACE1005539	659	R-PLACE1005539	1410
PLACE 1005544	F-PLACE1005544	660	R-PLACE1005544	1411
PLACE 1005569	F-PLACE1005569	661	R-PLACE1005569	1412
PLACE 1005601	F-PLACE1005601	662	R-PLACE1005601	1413
PLACE 1005660	F-PLACE1005660	663	R-PLACE1005660	1414
PLACE 1005669	F-PLACE1005669	664	R-PLACE1005669	1415
PLACE 1005682	F-PLACE1005682	665	R-PLACE1005682	1416
PLACE 1005725	F-PLACE1005725	666	R-PLACE1005725	1417
PLACE 1005736	F-PLACE1005736	667	R-PLACE1005736	1418
PLACE 1005745	F-PLACE1005745	668	R-PLACE1005745	1419
PLACE 1005768	F-PLACE1005768	669	R-PLACE1005768	1420
PLACE1005815	F-PLACE1005815	670	R-PLACE1005815	1421
PLACE 1005878	F-PLACE1005878	671	R-PLACE1005878	1422

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
PLACE 1005927	F-PLACE1005927	672	R-PLACE1005927	1423
PLACE 1006071	F-PLACE1006071	673	R-PLACE1006071	1424
PLACE 1006073	F-PLACE1006073	674	R-PLACE1006073	1425
PLACE 1006079	F-PLACE1006079	675	R-PLACE1006079	1426
PLACE 1006093	F-PLACE1006093	676	R-PLACE1006093	1427
PLACE 1006208	F-PLACE1006208	677	R-nnnnnnnnnnn	1428
PLACE 1006219	F-PLACE1006219	678	R-PLACE1006219	1429
PLACE 1006277	F-PLACE1006277	679	R-PLACE1006277	1430
PLACE 1006290	F-PLACE1006290	680	R-PLACE1006290	1431
PLACE 1006443	F-PLACE1006443	681	R-PLACE1006443	1432
PLACE 1006515	F-PLACE1006515	682	R-PLACE1006515	1433
PLACE 1006716	F-PLACE1006716	683	R-PLACE1006716	1434
PLACE 1006786	F-PLACE1006786	684	R-PLACE1006786	1435
PLACE 1006809	F-PLACE1006809	685	R-PLACE1006809	1436
PLACE 1006959	F-PLACE1006959	686	R-PLACE1006959	1437
PLACE 1007028	F-PLACE1007028	687	R-PLACE1007028	1438
PLACE 1007040	F-PLACE1007040	688	R-PLACE1007040	1439
PLACE 1007077	F-PLACE1007077	689	R-PLACE1007077	1440
PLACE 1007081	F-PLACE1007081	690	R-PLACE1007081	1441
PLACE 1007096	F-PLACE1007096	691	R-PLACE1007096	1442
PLACE 1007296	F-PLACE1007296	692	R-PLACE1007296	1443
PLACE 1007591	F-PLACE1007591	693	R-PLACE1007591	1444
PLACE1007626	F-PLACE1007626	694	R-PLACE1007626	1445
PLACE 1007702	F-PLACE1007702	695	R-PLACE1007702	1446
PLACE1007845	F-PLACE1007845	696	R-PLACE1007845	1447
PLACE1007881	F-PLACE1007881	697	R-PLACE1007881	1448
PLACE 1007971	F-PLACE1007971	698	R-PLACE1007971	1449
PLACE 1008282	F-PLACE1008282	699	R-PLACE1008282	1450
PLACE 1008297	F-PLACE1008297	700	R-PLACE1008297	1451
PLACE 1008359	F-PLACE1008359	701	R-PLACE1008359	1452
PLACE 1008469	F-PLACE1008469	702	R-PLACE1008469	1453
PLACE 1008549	F-PLACE1008549	703	R-PLACE1008549	1454
PLACE 1008657	F-PLACE1008657	704	R-PLACE1008657	1455
PLACE 1008716	F-PLACE1008716	705	R-PLACE1008716	1456
PLACE 1008744	F-PLACE1008744	706	R-PLACE1008744	1457
PLACE 1008984	F-PLACE1008984	707	R-PLACE1008984	1458
PLACE 1008985	F-PLACE1008985	708	R-PLACE1008985	1459
PLACE 1009067	F-PLACE1009067	709	R-PLACE1009067	1460
PLACE 1009196	F-PLACE1009196	710	R-PLACE1009196	1461
PLACE 1009279	F-PLACE1009279	711	R-PLACE1009279	1462
PLACE 1009527	F-PLACE1009527	712	R-PLACE1009527	1463
PLACE 1009546	F-PLACE1009546	713	R-PLACE1009546	1464
PLACE 1009600	F-PLACE1009600	714	R-PLACE1009600	1465
PLACE 1009735	F-PLACE1009735	715	R-PLACE1009735	1466
PLACE 1009982	F-PLACE1009982	716	R-nnnnnnnnnnn	1467
PLACE1010011	F-PLACE1010011	717	R-PLACE1010011	1468
PLACE1010078	F-PLACE1010078	718	R-PLACE1010078	1469
PLACE1010081	F-PLACE1010081	719	R-PLACE1010081	1470

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
PLACE 1010251	F-PLACE1010251	720	R-PLACE1010251	1471
PLACE1010445	F-PLACE1010445	721	R-PLACE1010445	1472
PLACE 1010713	F-PLACE1010713	722	R-PLACE1010713	1473
PLACE 1010784	F-PLACE1010784	723	R-PLACE1010784	1474
PLACE 1010827	F-PLACE1010827	724	R-PLACE1010827	1475
PLACE 1010968	F-PLACE1010968	725	R-PLACE1010968	1476
PLACE 1011045	F-PLACE1011045	726	R-PLACE1011045	1477
PLACE1011116	F-PLACE1011116	727	R-PLACE1011116	1478
PLACE1011181	F-PLACE1011181	728		
PLACE1011236	F-PLACE1011236	729	R-PLACE1011236	1479
PLACE 1011364	F-PLACE1011364	730	R-PLACE1011364	1480
PLACE 1 011407	F-PLACE1011407	731	R-PLACE1011407	1481
PLACE1011516	F-PLACE1011516	732	R-PLACE1011516	1482
PLACE 1011708	F-PLACE1011708	733	R-PLACE1011708	1483
PLACE 1011824	F-PLACE1011824	734	R-PLACE1011824	1484
PLACE 1011978	F-PLACE1011978	735	R-PLACE1011978	1485
PLACE2000118	F-PLACE2000118	736	R-PLACE2000118	1486
PLACE2000219	F-PLACE2000219	737	R-PLACE2000219	1487
PLACE3000181	F-PLACE3000181	738	R-PLACE3000181	1488
PLACE3000213	F-PLACE3000213	739	R-PLACE3000213	1489
PLACE4000354	F-PLACE4000354	740	R-PLACE4000354	1490
PLACE4000455	F-PLACE4000455	741	R-PLACE4000455	1491
SKNMC1000004	F-SKNMC1000004	742		
SKNMC1000014	F-SKNMC1000014	743		
SKNMC1000082	F-SKNMC1000082	744		
THYRO1000036	F-THYRO1000036	745	R-THYRO1000036	1492
THYRO1000061	F-THYRO1000061	746	R-THYRO1000061	1493
THYRO1000099	F-THYRO1000099	747	R-THYRO1000099	1494
THYRO1000196	F-THYRO1000196	748	R-THYRO1000196	1495
THYRO1000400	F-THYRO1000400	749	R-THYRO1000400	1496
THYRO1000580	F-THYRO1000580	750	R-THYRO1000580	1497
THYRO1000584	F-THYRO1000584	751	R-THYRO1000584	1498
THYRO1000678	F-THYRO1000678	752	R-THYRO1000678	1499
THYRO1000776	F-THYRO1000776	753	R-THYRO1000776	1500
THYRO1000795	F-THYRO1000795	754	R-THYRO1000795	1501
THYRO1000846	F-THYRO1000846	755	R-THYRO1000846	1502
THYRO1000866	F-THYRO1000866	756	R-THYRO1000866	1503
THYRO1000956	F-THYRO1000956	757	R-THYRO1000956	1504
THYRO1000964	F-THYRO1000964	758	R-THYRO1000964	1505
THYRO1000999	F-THYRO1000999	759	R-THYRO1000999	1506
THYRO1001063	F-THYRO1001063	760	R-THYRO1001063	1507
THYRO1001071	F-THYRO1001071	761	R-THYRO1001071	1508
THYR01001102	F-THYRO1001102	762	R-THYRO1001102	1509
THYRO1001113	F-THYRO1001113	763	R-THYRO1001113	1510
THYRO1001128	F-THYRO1001128	764	R-THYRO1001128	1511
THYRO1001205	F-THYRO1001205	765	R-THYRO1001205	1512
THYRO1001237	F-THYRO1001237	766	R-THYRO1001237	1513
THYRO1001242	F-THYRO1001242	767	R-THYRO1001242	1514

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
THYRO1001266	F-THYRO1001266	768	R-THYRO1001266	1515
THYRO1001327	F-THYRO1001327	769	R-THYRO1001327	1516
THYRO1001456	F-THYRO1001456	770	R-THYRO1001456	1517
THYRO1001457	F-THYRO1001457	771	R-THYRO1001457	1518
THYRO1001471	F-THYRO1001471	772	R-THYRO1001471	1519
THYRO1001478	F-THYRO1001478	773	R-THYRO1001478	1520
THYRO1001495	F-THYRO1001495	774	R-THYRO1001495	1521
THYRO1001523	F-THYRO1001523	775	R-THYRO1001523	1522
THYRO1001529	F-THYRO1001529	776	R-THYRO1001529	1523
THYRO1001593	F-THYRO1001593	777	R-THYRO1001593	1524
THYRO1001608	F-THYRO1001608	778	R-THYRO1001608	1525
THYRO1001641	F-THYRO1001641	779	R-THYRO1001641	1526
THYRO1001700	F-THYRO1001700	780	R-THYRO1001700	1527
THYRO1001702	F-THYRO1001702	781	R-THYRO1001702	1528
THYRO1001725	F-THYRO1001725	782	R-THYRO1001725	1529
THYRO1001770	F-THYRO1001770	783	R-THYRO1001770	1530
THYRO1001803	F-THYRO1001803	784	R-THYRO1001803	1531
Y79AA1000030	F-Y79AA1000030	785	R-Y79AA1000030	1532
Y79AA1000127	F-Y79AA1000127	786	R-Y79AA1000127	1533
Y79AA1000207	F-Y79AA1000207	787	R-Y79AA1000207	1534
Y79AA1000226	F-Y79AA1000226	788	R-Y79AA1000226	1535
Y79AA1000270	F-Y79AA1000270	789	R-Y79AA1000270	1536
Y79AA1000426	F-Y79AA1000426	790	R-Y79AA1000426	1537
Y79AA1000521	F-Y79AA1000521	791	R-Y79AA1000521	1538
Y79AA1000750	F-Y79AA1000750	792	R-Y79AA1000750	1539
Y79AA1000776	F-Y79AA1000776	793	R-Y79AA1000776	1540
Y79AA1000777	F-Y79AA1000777	794	R-Y79AA1000777	1541
Y79AA1000876	F-Y79AA1000876	795	R-Y79AA1000876	1542
Y79AA1000888	F-Y79AA1000888	796		
Y79AA1000959	F-Y79AA1000959	797	R-Y79AA1000959	1543
Y79AA1000967	F-Y79AA1000967	798	R-Y79AA1000967	1544
Y79AA1001013	F-Y79AA1001013	799	R-Y79AA1001013	1545
Y79AA1001056	F-Y79AA1001056	800	R-Y79AA1001056	1546
Y79AA1001062	F-Y79AA1001062	801	R-Y79AA1001062	1547
Y79AA1001090	F-Y79AA1001090	802	R-Y79AA1001090	1548
Y79AA1001212	F-Y79AA1001212	803	R-Y79AA1001212	1549
Y79AA1001264	F-Y79AA1001264	804	R-Y79AA1001264	1550
Y79AA1001272	F-Y79AA1001272	805	R-Y79AA1001272	1551
Y79AA1001328	F-Y79AA1001328	806	R-Y79AA1001328	1552
Y79AA1001426	F-Y79AA1001426	807	R-Y79AA1001426	1553
Y79AA1001427	F-Y79AA1001427	808		
Y79AA1001430	F-Y79AA1001430	809	R-Y79AA1001430	1554
Y79AA1001523	F-Y79AA1001523	810	R-Y79AA1001523	1555
Y79AA1001530	F-Y79AA1001530	811	R-Y79AA1001530	1556
Y79AA1001592	F-Y79AA1001592	812	R-Y79AA1001592	1557
Y79AA1001727	F-Y79AA1001727	813	R-Y79AA1001727	1558
Y79AA1001787	F-Y79AA1001787	814	R-Y79AA1001787	1559
Y79AA1001793	F-Y79AA1001793	815		

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
Y79AA1001795	F-Y79AA1001795	816	R-Y79AA1001795	1560
Y79AA1001799	F-Y79AA1001799	817	R-Y79AA1001799	1561
Y79AA1001803	F-Y79AA1001803	818	R-Y79AA1001803	1562
Y79AA1001863	F-Y79AA1001863	819	R-Y79AA1001863	1563
Y79AA1002022	F-Y79AA1002022	820	R-Y79AA1002022	1564
Y79AA1002058	F-Y79AA1002058	821		
Y79AA1002121	F-Y79AA1002121	822	R-nnnnnnnnnnnn	1565
Y79AA1002129	F-Y79AA1002129	823	R-nnnnnnnnnnnn	1566
Y79AA1002213	F-Y79AA1002213	824	R-Y79AA1002213	1567
Y79AA1002334	F-Y79AA1002334	825	R-Y79AA1002334	1568
Y79AA1002373	F-Y79AA1002373	826	R-Y79AA1002373	1569
Y79AA1002376	F-Y79AA1002376	827	R-Y79AA1002376	1570
Y79AA1002378	F-Y79AA1002378	828	R-Y79AA1002378	1571
Y79AA1002381	F-Y79AA1002381	829	R-Y79AA1002381	1572
NT2RP2006580	F-NT2RP2006580	2545	R-NT2RP2006580	2546

The sequence name starting from "F" means the name of 5'-end sequence, and the sequence name starting from "R" means the name of 3'-end sequence. A blank indicates that the 3'-end sequence corresponding to the 5'-end sequence has not been determined in the clone.

[0018] Furthermore, the present invention relates to the use of the above primers, as described below.

(4) A polynucleotide which can be synthesized with the primer set of (2) or (3).
(5) A polynucleotide comprising a coding region in the polynucleotide of (4).
(6) A substantially pure protein encoded by polynucleotide of (4).
(7) A partial peptide of the protein of (6).

[0019] In addition, the present invention comprises a polynucleotide described below and a protein encoded by the polynucleotide.

(8) An isolated polynucleotide selected from the group consisting of

(a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the SEQ ID NOs in Table 370;
(b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence set forth in any one of the SEQ ID NOs in Table 370;
(c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence selected from the amino acid sequences set forth in the SEQ ID NOs in Table 370, in which one or more amino acids are substituted, deleted, inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino acid sequence selected from the amino acid sequences set forth in the SEQ ID NOs in Table 370;
(d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the nucleotide sequences set forth in the SEQ ID NOs in Table 370, and that comprises a nucleotide sequence encoding a protein functionally equivalent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences set forth in the SEQ ID NOs in Table 370;
(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein encoded by the polynucleotide of (a) to (d);
(f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence set forth in any one of the SEQ ID NOs in Table 370.

(9). A substantially pure protein encoded by the polynucleotide of (8).
(10) An antibody against the protein or peptide of any one of (6), (7), and (9).
(11) A vector comprising the polynucleotide of (5) or (8).

(12) A transformant carrying the polynucleotide of (5) or (8), or the vector of (11).
(13) A transformant expressively carrying the polynucleotide of (5) or (8), or the vector of (11).
(14) A method for producing the protein or peptide of any one of (6), (7), and (9), comprising culturing the transformant of (13) and recovering the expression product.
(15) An oligonucleotide comprising; the nucleotide sequence set forth in any one of the SEQ ID NOs in Table 370 or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.
(16) Use of the oligonucleotide of (15) as a primer for synthesizing a polynucleotide.
(17) Use of the oligonucleotide of (15) as a probe for detecting a gene.
(18) An antisense polynucleotide against the polynucleotide of (8), or the portion thereof.
(19) A method for synthesizing a polynucleotide, the method comprising:

a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of (2) or (3), or the primer of (16); and
b) recovering the synthesized product.

(20) The method of (19), wherein the cDNA library is obtainable by oligo-capping method.
(21) The method of (19), wherein the complementary strand is obtainable by PCR.
(22) A method for detecting the polynucleotide of (8), the method comprising:

a) incubating a target polynucleotide with the oligonucleotide of (15) under the conditions where hybridization occurs, and
b) detecting the hybridization of the target polynucleotide with the oligonucleotide of (15).

(23) A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences set forth in the SEQ ID NOs in Table 370 and/or the amino acid sequences set forth in the SEQ ID NOs in Table 370, or a medium on which the database is stored.

[0020] Any patents, patent applications, and publications cited herein are incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0021]

Figure 1 shows the restriction maps of vectors pME18SFL3 and pUC19FL3.
Figure 2 shows the reproducibility of gene expression analysis. The ordinate and the abscissa show the intensities of gene expression obtained in experiments different from each other.
Figure 3 shows the detection limit in gene expression analysis. The intensity of expression is shown in the ordinate, and the concentration (μg/ml) of the probe used is shown in the abscissa.

DETAILED DESCRIPTION OF THE INVENTION

[0022] Herein, "polynucleotide" is defined as a molecule in which multiple nucleotides are polymerized. There are no limitations in the number of the polymerized nucleotides. In case that the polymer contains relatively low number of nucleotides, it is also described as an "oligonucleotide". The polynucleotide or the oligonucleotide of the present invention can be a natural or chemically synthesized product. Alternatively, it can be synthesized using a template DNA by an enzymatic reaction such as PCR.
[0023] All the cDNA provided by the invention are full-length cDNA. Herein, a "full-length cDNA" is defined as a cDNA which contains both ATG codon (the translation start site) and the stop codon. Accordingly, the untranslated regions, which are originally found in the upstream or downstream of the protein coding region in natural mRNA, may or may not be contained.
An "isolated polynucleotide" is a polynucleotide the structure of which is not identical to that of any naturally occurring nucleic acid or to that of any fragment of a naturally occurring genomic nucleic acid spanning more than three separate genes. The term therefore covers, for example,

(a) a DNA which has the sequence of part of a naturally occurring genomic DNA molecule but is not flanked by both of the coding sequences that flank that part of the molecule in the genome of the organism in which it naturally occurs;

(b) a nucleic acid incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA;
(c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and
(d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion protein. Specifically excluded from this definition are nucleic acids present in mixtures of different (i) DNA molecules, (ii) transfected cells, or (iii) cell clones: e.g., as these occur in a DNA library such as a cDNA or genomic DNA library.

[0024] The term "substantially pure" as used herein in reference to a given polypeptide means that the protein or polypeptide is substantially free from other biological macromolecules. The substantially pure protein or polypeptide is at least 75% (e.g., at least 80, 85, 95, or 99%) pure by dry weight. Purity can be measured by any appropriate standard method, for example, by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.
[0025] All the clones of the present invention (830 clones) are novel and covering full-length, and also predicted to encode any of the following functional protein:

secretory proteins,
membrane proteins,
proteins associated to signal transduction (signal transduction-associated proteins; e.g. protein kinases, etc.),
proteins associated to a glycoprotein (glycoprotein-associated proteins),
proteins associated with transcription (transcription-associated proteins),
proteins associated with diseases (disease-associated proteins),
or, enzymes and/or metabolism-associated proteins, cell division- and/or cell proliferation-associated proteins, cytoskeleton-associated proteins, nuclear proteins, DNA-and/or RNA-binding proteins, ATP- and/or GTP-binding proteins, protein synthesis- and/or protein transport-associated proteins, and cellular defense-associated proteins.

[0026] Furthermore, all the cDNA clones of the present invention can be characterized as follows:

(1) a cDNA that is obtained by the oligo-capping method, which provides cDNA with high fullness ratio. The cDNA was selected by the score in the ATGpr (described as ATGpr1, as well), which is a program for prediction of the fullness of the 5'-end of cDNA based on the features of the 5'-end sequence. In addition, the PSORT, which is a program for prediction of the existence of the signal sequence selected, cDNA that contains a signal sequence in the 5'-end, or transmembrane region in the protein coding region. Furthermore, the homology search with the 5'-end sequences confirmed that, the selected clones were not identical to any of the known human mRNA (namely novel);
or,
(2) a cDNA that is obtained by the oligo-capping method, which provides cDNA with high fullness ratio. The cDNA was selected by the score in the ATGpr, which is a program for prediction of the fullness of the 5'-end based on the features of the 5'-end sequence. Furthermore, the a cDNA that has relative homology with an amino acid sequence of a protein with known functions was selected by the BLAST search (Altschul S.F., Gish W., Miller W., Myers E.W., and Lipman D.J. (1990) J. Mol. Biol. 215: 403-410 ; Gish W., and States D.J. (1993) Nature Genet. 3: 266-272) on the SwissProt database using the 5'-end sequence. In addition, the homology search using the 5'-end sequence confirmed that the selected clones were not identical to any of the known human mRNA (namely novel).

[0027] All clones are obtainable as a full-length clone by such a method as PCR (Current Protocols in Molecular Biology, Ausubel et al. edit, (1987) John Wiley & Sons, Section 6.1-6.4) using both the 5'- and 3'-end sequences, or using the 5'-end sequence and an oligo-dT primer that corresponds to the polyA sequence.
[0028] Specifically, PCR can be performed using an oligonucleotide that has 15 nucleotides longer, and specifically hybridizes with the complementary strand of the polynucleotide that contains the nucleotide sequence selected from the 5'-end sequences shown in Table 1 (SEQ ID NO: 1-829, and SEQ ID NO: 2545), and an oligo-dT primer as a 5'-, and 3'-primer, respectively. The length of the primers is usually 15-100 bp, and favorably between 15-35 bp. In case of LA PCR, which is described below, the primer length of 25-35 bp may provide a good result.
[0029] A method to design a primer that enables a specific amplification based on the given nucleotide sequence is known to those skilled in the art (Current Protocols in Molecular Biology, Ausubel et al. edit, (1987) John Wiley & Sons, Section 6.1-6.4). In designing a primer based on the 5'-end sequence, the primer is designed so as that, in principle, the amplification products will include the translation start site. Accordingly, in case that a given 5'-end nucleotide sequence is the 5'-untranslated region (5'UTR), any part of the sequence can be used as a 5'-primer as far as the specificity toward the target cDNA is insured. The translation start site can be predicted using a known method such

as the ATGpr as described below.

[0030] When synthesizing a polynucleotide, the target nucleotide sequence to be amplified can extend to several thousand bp in some cDNA. However, it is possible to amplify such a long nucleotides by using such as LA PCR (Long and Accurate PCR). It is advantageous to use LA PCR when synthesizing long DNA In LA PCR, in which a special DNA polymerase having 3' □5' exonuclease activity is used, misincorporated nucleotides can be removed. Accordingly, accurate synthesis of the complementary strand can be achieved even with a long nucleotide sequence. By using LA PCR, it is reported that amplification of a nucleotide with 20 kb longer can be achieved under desirable condition (Takeshi Hayashi (1996) Jikken-Igaku Bessatsu, "Advanced Technologies in PCR" Youdo-sha).

[0031] A template DNA for synthesizing the cDNA of the present invention can be obtained by using cDNA libraries that are prepared by various methods. The full-length cDNA clones obtained here are those with high fullness ratio, which were obtained using a combination of (1) a method to prepare a full-length-enriched cDNA library using the oligo-capping method, and (2) an estimation system for fullness using the 5'-end sequence (selection based on the estimation by the ATGpr after removing clones that are non-full-length compared to the ESTs). However, it is possible to easily obtain a full-length cDNA by using the primers that are provided by the present invention, not by the above described specialized method.

[0032] The problem with the cDNA libraries prepared by the known methods or commercially available is that mRNA contained in the libraries has very low fullness ratio. Thus, it is difficult to screen full-length cDNA clone directly from the library using ordinary cloning methods. The present invention has revealed a primer that is capable of synthesizing a full-length cDNA. If provided with primers, it is possible to synthesize a target full-length cDNA by using enzymatic reactions such as PCR. In particular, a full-length-enriched cDNA library, synthesized by methods such as oligo-capping, is desirable to synthesize a full-length cDNA with more reliability.

[0033] Once the nucleotide sequences of the full-length cDNAs obtained in the present invention is determined, it is possible to predict the functions of the proteins encoded by the cDNA clones, for example, by searching the databases such as GenBank (http://www.ncbi.nlm.nih.gov/web/GenBank/), Swiss-Prot (http://www.ebi.ac.uk/ebi_docsSwiss-Prot_db/swisshome.html), UniGene (http://www.ncbi.nlm.nih.gov/UniGene) for homologies of the cDNAs, or by searching the amino acid sequences deduced from the full-length nucleotide sequences for signal sequence by using software such as PSORT (K. Nakai & M. Kanehisa, Genomics, 14: 897-991 (1992), for transmembrane region by using software such as SOSUI (T. Hirokawa et al., Bioinformatics, 14:378-379 (1998); Mitsui Knowledge Industry Co., Ltd.) or for motif by using software such as Pfam (http://www.sanger.ac.uk/Software/Pfam/index.shtml) or PROSITE (http://www.expasy.ch/prosite). As a matter of course, the functions are often predictable by using partial sequence information (preferably 300 nucleotides or more) instead of the full-length nucleotide sequences. However, the result of the prediction obtained by using partial sequence information does not always agree with the result obtained by using full-length nucleotide sequence, and thus it is needless to say that the prediction of function is preferably performed based on the full-length nucleotide sequences.

[0034] Homology search using each of GenBank, Swiss-Prot and UniGene was performed for the 826 clones whose full-length nucleotide sequences had been determined (HEMBA1005337, NT2RM1000407, NT2RM2001767, and NT2RP3003939 are not full-length). The amino acid sequences deduced from the full-length nucleotide sequences were searched for functional domains by using analytical software programs, PSORT, SOSUI and Pfam. Based on the results, proteins encoded by the cDNA clones were grouped into some categories and their functions were predicted.

[0035] The following 437 clones were categorized into secretory and/or membrane proteins. The clones categorized into secretory and/or membrane proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "growth factor", "cytokine", "hormone", "signal", "transmembrane", "membrane", "extracellular matrix", "receptor", "G-protein coupled receptor", "ionic channel", "voltage-gated channel", "calcium channel", "cell adhesion", "collagen" or "connective tissue"; those which matched the data, suggesting that the proteins are secretory and/or membrane proteins; or those which matched with the full-length sequences of GenBank or UniGene database similar description; and, further, those predicted to have an N-terminal signal sequence or a transmembrane region as a result of domain search for the amino acid sequences deduced from the full-length nucleotide sequences.

BNGH41000020, BNGH41000087, BNGH41000091, HEMBA1000121, HEMBA1000128, HEMBA1000349, HEMBA1000477, HEMBA1000590, HEMBA1000713, HEMBA1000732, HEMBA1000745, HEMBA1000835, HEMBA1000940, HEMBA1000962, HEMBA1001221, HEMBA1001228, HEMBA1001621, HEMBA1002131, HEMBA1002163, HEMBA1002167, HEMBA1002178, HEMBA1002195, HEMBA1002227, HEMBA1002420, HEMBA1002421, HEMBA1002767, HEMBA1003047, HEMBA1003101, HEMBA1003230, HEMBA1003392, HEMBA1003530, HEMBA1003602, HEMBA1003732, HEMBA1003945, HEMBA1004110, HEMBA1004250, HEMBA1004391, HEMBA1004444, HEMBA1004454, HEMBA1004505, HEMBA1004797, HEMBA1004982, HEMBA1005070, HEMBA1005449, HEMBA1005522, HEMBA1005545, HEMBA1005698, HEMBA1005945, HEMBA1006171, HEMBA1006299, HEMBA1006311, HEMBA1006335, HEMBA1006357, HEMBA1006430, HEMBA1006482, HEMBA1006707, HEMBA1006724, HEMBA1006749, HEMBA1006902, HEMBA1006960, HEMBA1007241, HEMBB1000407, HEMBB1000447, HEMBB1000567, HEMBB1000679, HEMBB1000881,

HEMBB1001026, HEMBB1001048, HEMBB1001407, HEMBB1001530, HEMBB1001573, HEMBB1001847, HEMBB1001978, HEMBB1002041, HEMBB1002162, HEMBB1002245, HEMBB1002427, HEMBB1002693, MAMMA1000102, MAMMA1000106, MAMMA1000118, MAMMA1000141, MAMMA1000204, MAMMA1000226, MAMMA1000457, MAMMA1000473, MAMMA1000496, MAMMA1000591, MAMMA1000681, MAMMA1000810, MAMMA1000986, MAMMA1000994, MAMMA1001043, MAMMA1001141, MAMMA1001237, MAMMA1001344, MAMMA1001418, MAMMA1001893, MAMMA1001957, MAMMA1001978, MAMMA1002070, MAMMA1002091, MAMMA1002095, MAMMA1002165, MAMMA1002234, MAMMA1002586, MAMMA1002633, MAMMA1003126, NT2RM1000462, NT2RM1000542, NT2RM1000580, NT2RM1000855, NT2RM1000858, NT2RM1000899, NT2RM2000241, NT2RM2000410, NT2RM2000423, NT2RM2000565, NT2RM2001626, NT2RM2001792, NT2RM2001939, NT2RM2001941, NT2RM4000198, NT2RM4000284, NT2RM4000417, NT2RM4000444, NT2RM4000587, NT2RM4000593, NT2RM4000648, NT2RM4000761, NT2RM4000997, NT2RM4001325, NT2RM4001735, NT2RM4001768, NT2RM4001843, NT2RM4002352, NT2RP1000050, NT2RP1000181, NT2RP1000261, NT2RP1000300, NT2RP1000325, NT2RP1000448, NT2RP1000551, NT2RP1000613, NT2RP1000981, NT2RP1001004, NT2RP1001563, NT2RP2000479, NT2RP2000533, NT2RP2000616, NT2RP2000649, NT2RP2000663, NT2RP2000694, NT2RP2000818, NT2RP2000903, NT2RP2001200, NT2RP2001276, NT2RP2001480, NT2RP2001495, NT2RP2001514, NT2RP2001755, NT2RP2001915, NT2RP2001956, NT2RP2002063, NT2RP2002188, NT2RP2002232, NT2RP2002527, NT2RP2002533, NT2RP2002721, NT2RP2002824, NT2RP2002942, NT2RP2002976, NT2RP2003042, NT2RP2003210, NT2RP2003383, NT2RP2003390, NT2RP2003469, NT2RP2003593, NT2RP2003655, NT2RP2003664, NT2RP2003950, NT2RP2004179, NT2RP2004205, NT2RP2004495, NT2RP2004524, NT2RP2004556, NT2RP2004606, NT2RP2004648, NT2RP2004794, NT2RP2005027, NT2RP2005163, NT2RP2005181, NT2RP2005378, NT2RP2005463, NT2RP2005541, NT2RP2005597, NT2RP2005666, NT2RP2005883, NT2RP2005994, NT2RP2006004, NT2RP2006042, NT2RP2006269, NT2RP1006512, NT2RP2006580, NT2RP3000169, NT2RP3000171, NT2RP3000304, NT2RP3000436, NT2RP3000460, NT2RP3000616, NT2RP3000676, NT2RP3000721, NT2RP3000818, NT2RP3000907, NT2RP3000921, NT2RP3001012, NT2RP3001159, NT2RP3001195, NT2RP3001240, NT2RP3001271, NT2RP3001322, NT2RP3001388, NT2RP3001560, NT2RP3001592, NT2RP3001650, NT2RP3001738, NT2RP3001858, NT2RP3002015, NT2RP3002160, NT2RP3002311, NT2RP3002342, NT2RP3002411, NT2RP3002737, NT2RP3002790, NT2RP3002836, NT2RP3002900, NT2RP3002958, NT2RP3003000, NT2RP3003076, NT2RP3003354, NT2RP3003532, NT2RP3003535, NT2RP3003614, NT2RP3004025, NT2RP3004075, NT2RP3004083, NT2RP3004130, NT2RP3004133, NT2RP3004309, NT2RP3004345, NT2RP3004406, NT2RP3004481, NT2RP3004552, NT2RP3004625, NT2RP3004647, NT2RP4001001, NT2RP4001009, NT2RP4001467, NT2RP4001879, NT2RP4002187, NT2RP4002451, NT2RP4002750, OVARC1000003, OVARC1000105, OVARC1000298, OVARC1000307, OVARC1000313, OVARC1000410, OVARC1000439, OVARC1000553, OVARC1000811, OVARC1000873, OVARC1000956, OVARC1001030, OVARC1001163, OVARC1001336, OVARC1001570, OVARC1001607, OVARC1001725, OVARC1001991, PLACE1000033, PLACE1000231, PLACE1000560, PLACE1000740, PLACE1000912, PLACE1000914, PLACE1000927, PLACE1001016, PLACE1001123, PLACE1001183, PLACE1001231, PLACE1001340, PLACE1001401, PLACE1001407, PLACE1001464, PLACE1001516, PLACE1001536, PLACE1001564, PLACE1001655, PLACE1001795, PLACE1001836, PLACE1001918, PLACE1001949, PLACE1002080, PLACE1002095, PLACE1002355, PLACE1002374, PLACE1002518, PLACE1002547, PLACE1002726, PLACE1002905, PLACE1002911, PLACE1002967, PLACE1003407, PLACE1003573, PLACE1003737, PLACE1003772, PLACE1003839, PLACE1003845, PLACE1003852, PLACE1004279, PLACE1004282, PLACE1004441, PLACE1004450, PLACE1004482, PLACE1004520, PLACE1004630, PLACE1004657, PLACE1004648, PLACE1004816, PLACE1005003, PLACE1005005, PLACE1005031, PLACE1005383, PLACE1005410, PLACE1005426, PLACE1005544, PLACE1005569, PLACE1005660, PLACE1005725, PLACE1005745, PLACE1005878, PLACE1005927, PLACE1006071, PLACE1006093, PLACE1006208, PLACE1006277, PLACE1006290, PLACE1006443, PLACE1006716, PLACE1006809, PLACE1006959, PLACE1007081, PLACE1007096, PLACE1007296, PLACE1007626, PLACE1007845, PLACE1007881, PLACE1008359, PLACE1008469, PLACE1008716, PLACE1008744, PLACE1008985, PLACE1009067, PLACE1009196, PLACE1009279, PLACE1009527, PLACE1009546, PLACE1009600, PLACE1009982, PLACE1010011, PLACE1010078, PLACE1010251, PLACE1010445, PLACE1010713, PLACE1010784, PLACE1010827, PLACE1010968, PLACE1011116, PLACE1011181, PLACE1011236, PLACE1011516, PLACE1011708, PLACE3000181, PLACE3000213, PLACE4000354, SKNMC1000004, SKNMC1000014, SKNMC1000082, THYRO1000036, THYRO1000099, THYRO1000196, THYRO1000400, THYRO1000584, THYRO1000678, THYPO1000776, THYRO1000795, THYRO1000956, THYRO1001102, THYRO1001113, THYRO1001205, THYRO1001237, THYRO1001242, THYRO1001266, THYRO1001327, THYRO1001456,

THYRO1001478, THYRO1001523, THYRO1001529, THYRO1001641, THYRO1001702, THYRO1001725, Y79AA1000207, Y79AA1000226, Y79AA1000270, Y79AA1000426, Y79AA1000521, Y79AA1000876, Y79AA1000888, Y79AA1000959, Y79AA1001013, Y79AA1001212, Y79AA1001264, Y79AA1001328, Y79AA1001426, Y79AA1001427, Y79AA1001430, Y79AA1001727, Y79AA1001787, Y79AA1001795, Y79AA1001799, Y79AA1001803, Y79AA1002022, Y79AA1002058, Y79AA1002129, Y79AA1002213, Y79AA1002373,

[0036] The following 146 clones were categorized into glycoprotein-associated proteins. The clones categorized into glycoprotein-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keyword "glycoprotein"; those which matched the data suggesting that the proteins are glycoprotein; or those which matched the full-length sequences of GenBank or UniGene database with similar description.

BNGH41000087, BNGH41000091, HEMBA1000349, HEMBA1000590, HEMBA1000745, HEMBA1000835, HEMBA1001221, HEMBA1001228, HEMBA1001621, HEMBA1002131, HEMBA1002178, HEMBA1002421, HEMBA1002767, HEMBA1003230, HEMBA1003392, HEMBA1004250, HEMBA1004391, HEMBA1004444, HEMBA1004505, HEMBA1005449, HEMBA1005522, HEMBA1005545, HEMBA1006707, HEMBA1006749, HEMBA1006902, HEMBB1000679, HEMBB1000881, HEMBB1001048, HEMBB1002120, HEMBB1002245, HEMBB1002427, MAMMA1000102, MAMMA1000591, MAMMA1000681, MAMMA1001043, MAMMA1001237, MAMMA1002070, MAMMA1002586, MAMMA1003126, NT2RM1000462, NT2RM1000580, NT2RM2001792, NT2RM2001818, NT2RM2001939, NT2RM2001941, NT2RM4000198, NT2RM4000284, NT2RM4000417, NT2RM4000648, NT2RM4000997, NT2RM4001325, NT2RM4002352, NT2RP1000613, NT2RP1000981, NT2RP1001004, NT2RP2000616, NT2RP2000694, NT2RP2000903, NT2RP2001480, NT2RP2001755, NT2RP2002533, NT2RP2003042, NT2RP2003210, NT2RP2004205, NT2RP2004606, NT2RP2005027, NT2RP2005181, NT2RP2005541, NT2RP2005597, NT2RP2005883, NT2RP2006004, NT2RP2006042, NT2RP2006269, NT2RP3000304, NT2RP3000616, NT2RP3000921, NT2RP3001650, NT2RP3002160, NT2RP3002737, NT2RP3002958, NT2RP3003000, NT2RP3003532, NT2RP3004130, NT2RP3004133, NT2RP3004481, NT2RP3004552, NT2RP3004640, NT2RP4000108, NT2RP4001467, NT2RP4002750, OVARC1000003, OVARC1000553, OVARC1000811, OVARC1000873, OVARC1001336, OVARC1001607, OVARC1001991, PLACE1000033, PLACE1000740, PLACE1001016, PLACE1001123, PLACE1001231, PLACE1001464, PLACE1001655, PLACE1001836, PLACE1002355, PLACE1002374, PLACE1002905, PLACE1002911, PLACE1003573, PLACE1003737, PLACE1003772, PLACE1003839, PLACE1004282, PLACE1004441, PLACE1004450, PLACE1004520, PLACE1004648, PLACE1005003, PLACE1005426, PLACE1006071, PLACE1006073, PLACE1006290, PLACE1007081, PLACE1007845, PLACE1008716, PLACE1008744, PLACE1008985, PLACE1010251, PLACE1010784, PLACE1010968, PLACE1011116, PLACE3000181, PLACE3000213, PLACE4000354, THYRO1000036, THYRO1000196, THYRO1000584, THYRO1000956, THYRO1001266, Y79AA1000270, Y79AA1000426, Y79AA1001727, Y79AA1001795, Y79AA1002022, Y79AA1002213,

[0037] The following 57 clones were categorized into signal transduction-associated proteins. The clones categorized into signal transduction-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "serine/threonine-protein kinase", "tyrosine-protein kinase" or "SH3 domain"; those which matched the data suggesting that the proteins are signal transduction-associated proteins (for example, "ADP-ribosylation factor"); or those which matched the full-length sequences of GenBank or UniGene database with similar description; and, further, those which was similarly predicted to be signal transduction-associated proteins based on the matching data of Pfam.

HEMBA1000006, HEMBA1002195, HEMBA1002227, HEMBA1002551, HEMBA1005084, HEMBA1005929, HEMBA1006658, HEMBA1006916, MAMMA1000881, MAMMA1001150, MAMMA1001310, MAMMA1002142, NT2RM2001902, NT2RP1001020, NT2RP1001031, NT2RP2001469, NT2RP2001529, NT2RP2001769, NT2RP2003179, NT2RP2003545, NT2RP2004670, NT2RP3000011, NT2RP3000022, NT2RP3000172, NT2RP3000201, NT2RP3000820, NT2RP3003527, NT2RP3003849, NT2RP3003874, NT2RP3004067, NT2RP4000634, NT2RP4000962, OVARC1000255, OVARC1000529, OVARC1000916, OVARC1001338, OVARC1001569, PLACE1002329, PLACE1003135, PLACE1003598, PLACE1005519, PLACE1006208, PLACE1008282, PLACE1008297, PLACE1010081, PLACE1011364, PLACE1011824, THYRO1001457, THYRO1001593, THYRO1001700, THYRO1001770, Y79AA1000777, Y79AA1000967, Y79AA1002376, Y79AA1002381, HEMBB1000668, NT2RM4001377

[0038] The following 81 clones were categorized into transcription-associated proteins. The clones categorized into transcription-associated proteins are those which keywords "transcription regulation", "zinc finger" or "homeobox" matched the full-length sequences of Swiss-Prot database; those which the matched the data suggesting that the proteins were transcription-associated proteins; or those which matched the full-length sequences of GenBank or UniGene database with similar description; and, further, those which was similarly predicted to be transcription-associated proteins based on the matching data of Pfam.

HEMBA1000462, HEMBA1000671, HEMBA1001297, HEMBA1001390, HEMBA1001886, HEMBA1002048, HEMBA1003120, HEMBA1003497, HEMBA1004785, HEMBA1005230, HEMBA1005246, HEMBA1006276, HEMBA1006572, HEMBA1007226, HEMBB1000106, HEMBB1000905, HEMBB1001959, HEMBB1002051, HEMBB1002661, MAMMA1001094, MAMMA1001532, MAMMA1001615, NT2RM1000789, NT2RM2000632, NT2RM2000773, NT2RM4000326, NT2RP1000271, NT2RP1000468, NT2RP2000092, NT2RP2000610, NT2RP2000712, NT2RP2000739, NT2RP2001538, NT2RP2001662, NT2RP2001817, NT2RP2001948, NT2RP2002564, NT2RP2002974, NT2RP2003138, NT2RP2003302, NT2RP2003940, NT2RP2004108, NT2RP2004847, NT2RP2005247, NT2RP2005391, NT2RP2005535, NT2RP2005774, NT2RP2005941, NT2RP2006092, NT2RP3000148, NT2RP3000232, NT2RP3000378, NT2RP3000652, NT2RP3001976, NT2RP3004090, NT2RP3004119, NT2RP3004294, OVARC1001049, OVARC1001086, OVARC1001132, OVARC1001807, PLACE1000258, PLACE1000442, PLACE1000907, PLACE1003529, PLACE1004166, PLACE1004168, PLACE1004887, PLACE1005250, PLACE1005682, PLACE1006079, PLACE1008549, PLACE1011407, PLACE1011978, THYRO1000580, Y79AA1000030, Y79AA1001090, Y79AA1001523, Y79AA1002334, Y79AA1002378, HEMBB1002302,

[0039] The following 85 clones were categorized into disease-associated proteins. The clones categorized into disease-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "disease mutation" or "syndrome"; those which matched the data suggesting that the proteins are disease-associated proteins; or those which matched the full-length sequences of Swiss-Prot database and GenBank or UniGene database where the matched sequences are those of genes or proteins which had been deposited in the database of Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/Omim/), which is a database of human genes and diseases.

BNGH41000020, HEMBA1000349, HEMBA1000590, HEMBA1000671, HEMBA1000835, HEMBA1001184, HEMBA1001228, HEMBA1001886, HEMBA1003120, HEMBA1004250, HEMBA1005246, HEMBA1005267, HEMBA1006707, HEMBA1006749, HEMBA1006902, HEMBA1006916, HEMBA1007013, HEMBB1002120, MAMMA1000204, MAMMA1002080, NT2RM2000632, NT2RM2001126, NT2RM2001558, NT2RP1000271, NT2RP1000465, NT2RP1000579, NT2RP2000447, NT2RP2000514, NT2RP2000739, NT2RP2001223, NT2RP2001529, NT2RP2001562, NT2RP2002674, NT2RP2003369, NT2RP2004108, NT2RP2004205, NT2RP2005535, NT2RP2005941, NT2RP2006004, NT2RP3000059, NT2RP3000125, NT2RP3000201, NT2RP3000232, NT2RP3000616, NT2RP3000677, NT2RP3000838, NT2RP3000921, NT2RP3001542, NT2RP3002286, NT2RP3002721, NT2RP3002737, NT2RP3002738, NT2RP3004481, OVARC1000208, OVARC1000275, OVARC1000331, OVARC1000410, OVARC1001086, OVARC1001132, OVARC1001607, OVARC1001725, OVARC1001952, PLACE1000258, PLACE1000442, PLACE1000907, PLACE1001100, PLACE1001500, PLACE1002905, PLACE1002967, PLACE1003407, PLACE1003428, PLACE1005005, PLACE1005239, PLACE1005815, PLACE1007028, PLACE1008716, PLACE1011407, PLACE1011978, PLACE2000118, THYPO1000580, THYRO1000866, THYRO1001071, THYRO1001478, Y79AA1001062, Y79AA1001530,

[0040] It is unclear, by the analyses so far, whether or not the remaining 212 clones encode proteins belonging to any of the categories of secretory and/or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins or disease-associated proteins. Nonetheless, it is still possible for these clones to encode secretory and/or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins, or disease-associated proteins. On the other hand, some of these clones can be presumed to have functions other than those as secretory and/or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins and disease-associated proteins.

[0041] Among the 212 clones, the following clones presumably belong to the categories of enzymes and/or metabolism-associated proteins, cell division- and/or cell proliferation-associated proteins, cytoskeleton-associated proteins, nuclear proteins, DNA- and/or RNA-binding proteins, ATP-and/or GTP-binding proteins, protein synthesis- and/or protein transport-associated proteins, or cellular defense-associated proteins, although it is unclear whether or not the clones belong to any of the categories of secretory and/or transmembrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins, and disease-associated proteins.

[0042] The following 10 clones presumably belong to the category of enzymes and/or metabolism-associated proteins. The clones herein defined as clones presumably belonging to the category of enzymes and/or metabolism-associated proteins matched data containing keywords such as "metabolism", "oxidoreductase" and "E.C. No. (Enzyme commission number)".

HEMBA1003315, HEMBB1002465, MAMMA1000614, NT2RP2000178, NT2RP2001388, NT2RP2001903, NT2RP2002304, NT2RP2005878, NT2RP3001685, PLACE1006219

[0043] The following 4 clones presumably belong to the category of cell division- and/or cell proliferation-associated proteins. The cDNA clones were herein defined as clones presumably belonging to the category of cell division- and/

or cell proliferation-associated proteins matched data containing keywords such as "cell division", "cell cycle", "mitosis", "chromosomal protein", "cell growth" and "apoptosis".
MAMMA1000403, NT2RM2000497, NT2RP2000394, Y79AA1002121

[0044] The following 6 clones presumably belong to the category of cytoskeleton-associated proteins. The cDNA clones were herein defined as clones presumably belonging to the category of cytoskeleton-associated proteins matched data containing keywords such as "structural protein", "cytoskeleton", "actin-binding" and "microtubules".
MAMMA 1001609, NT2RM2000589, NT2RP3000063, PLACE 1004078, PLACE 1004492, PLACE 1008657

[0045] The following 7 clones presumably belong to the category of nuclear proteins. The cDNA clones were herein defined as clones presumably belonging to the category of nuclear proteins matched data containing keywords such as "nuclear protein".
HEMBA1001878, HEMBA1002992, MAMMA1000614, NT2RM4000965, NT2RM2001738, NT2RP2001388, Y79AA1002121

[0046] The following 5 clones presumably belong to the category of DNA- and/or RNA-binding proteins. The cDNA clones were herein defined as clones presumably belonging to the category of DNA- and/or RNA-binding proteins matched data containing keywords such as "DNA-binding" and "RNA-binding".
HEMBA1003072, HEMBA1006770, HEMBA1007332, NT2RM2000497, Y79AA1002121

[0047] The following 7 clones presumably belong to the category of ATP- and/or GTP-binding proteins. The cDNA clones were herein defined as clones presumably belonging to the category of ATP- and/or GTP-binding proteins matched data containing keywords such as "ATP-binding" and "GTP-binding".
HEMBA1002316, MAMMA1001609, NT2RM2000306, NT2RM2000497, NT2RP2000178, NT2RP3003729, PLACE1004305

[0048] The following 7 clones presumably belong to the category of protein synthesis- and/or protein transport-associated proteins. The cDNA clones were herein defined as clones presumably belonging to the category of protein synthesis-associated and/or protein transport-associated proteins matched data containing keywords such as "translation regulation", "protein biosynthesis", "amino-acid biosynthesis", "ribosomal protein", "protein transport" and "signal recognition particle".
NT2RM4000965, NT2RP2005069, NT2RP3000481, NT2RP3000789, NT2RP4001877, OVARC1001833, OVARC1002058,

[0049] The following 1 clone presumably belongs to the category of cellular defense-associated proteins. The cDNA clones were herein defined as clones presumably belonging to the category of cellular defense-associated proteins matched data containing keywords such as "heat shock", "DNA repair" and "DNA damage".
PLACE1005539

[0050] Although it is unclear whether or not 26 out of 174 clones other than the above-mentioned clones belong to any of the above-described categories, these clones are predicted to have some functions, based on the homology search using their full-length sequences thereof. The clone names and the gene definitions found in the result of homology search are shown below, separated with a double-slash mark, //.

HEMBA1000634//Homo sapiens T-cell activation protein (PGR1) gene, complete cds.
HEMBA1002524//Human MHC Class I region proline rich protein mRNA, complete cds.
HEMBA1003399//MVP1 PROTEIN.
HEMBA1005489//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds.
HEMBB1000542//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.
MAMMA1000788//Bos taurus P14 (p14) mRNA, complete cds.
MAMMA1002128//ABC1 PROTEIN HOMOLOG PRECURSOR.
NT2RM2000514//Homo Sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.
NT2RM2000622//Mus musculus F-box protein FBL10 mRNA, partial cds.
NT2RM4000100//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.
NT2RP2005425//Homo sapiens mRNA for AKAP450 protein.
NT2RP3001170//Mus musculus activity-dependent neuroprotective protein (Adnp) mRNA, complete cds.
NT2RP3002571//Bos taurus mRNA for lyncein.
NT2RP3004557//Human Ki nuclear autoantigen mRNA, complete cds.
OVARC1001596//Homo sapiens Arf-like 2 binding protein BART1 mRNA, complete cds.
PLACE1002153//Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.
PLACE1003163//Homo sapiens DBI-related protein mRNA, complete cds.
PLACE1005736//Human mRNA for BAS-GRIP protein.
PLACE1007702//Mus musculus TRA1 mRNA, complete cds.
PLACE1011045//Homo sapiens E1-like protein mRNA, complete cds.

THYRO1000061//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.
THYRO1000964//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.
Y79AA1000776//Mus musculus mRNA for GSG1, complete cds.
Y79AA1001056//Homo sapiens MAID protein mRNA, complete cds.
Y79AA1001272//Homo sapiens retinoic acid repressible protein (RARG-1) mRNA, complete cds.
Y79AA1001793//Mus musculus mRNA for GSG1, complete cds.

[0051] So far, useful information for presuming the functions are unavailable for the remaining 148 clones, whose names are listed below.

HEMBA1000275, HEMBA1000300, HEMBA1000443, HEMBA1000875, HEMBA1000907, HEMBA1001272, HEMBA1001296, HEMBA1001563, HEMBA1002164, HEMBA1002239, HEMBA1002985, HEMBA1003294, HEMBA1003487, HEMBA1004007, HEMBA1004067, HEMBA1004085, HEMBA1004952, HEMBA1004971, HEMBA1005145, HEMBA1005430, HEMBA1005913, HEMBA1006016, HEMBA1006517, HEMBA1006544, HEMBA1006912, HEMBA1007057, HEMBA1007063, HEMBA1007291, HEMBB1000276, HEMBB1000309, HEMBB1000642, HEMBB1001200, HEMBB1001547, HEMBB1002039, HEMBB1002228, HEMBB1002663, MAMMA1000046, MAMMA1000449, MAMMA1000528, MAMMA1000652, MAMMA1000706, MAMMA1000814, MAMMA1001066, MAMMA1001284, MAMMA1001623, MAMMA1001634, MAMMA1001901, MAMMA1002087, MAMMA1002205, MAMMA1002224, NT2RM2000582, NT2RM2001643, NT2RM4000115, NT2RM4000295, NT2RM4001321, NT2RP1000002, NT2RP1000239, NT2RP1000679, NT2RP1000740, NT2RP1000903, NT2RP2000240, NT2RP2001878, NT2RP2001921, NT2RP2002015, NT2RP2002409, NT2RP2002510, NT2RP2003599, NT2RP2003931, NT2RP2004069, NT2RP2004141, NT2RP2004447, NT2RP2004837, NT2RP2005514, NT2RP2005632, NT2RP2005887, NT2RP2006099, NT2RP2006134, NT2RP3000427, NT2RP3000444, NT2RP3000645, NT2RP3000871, NT2RP3001044, NT2RP3001061, NT2RP3001754, NT2RP3002281, NT2RP3002324, NT2RP3002353, NT2RP3002409, NT2RP3002448, NT2RP3002664, NT2RP3002887, NT2RP3002983, NT2RP3003448, NT2RP3003469, NT2RP3003473, NT2RP3003559, NT2RP3003963, NT2RP3004000, NT2RP3004202, NT2RP3004321, NT2RP3004355, NT2RP3004374, NT2RP4002715, OVARC1000090, OVARC1000137, OVARC1000467, OVARC1000775, OVARC1000853, OVARC1000995, OVARC1001222, OVARC1001260, OVARC1001727, OVARC1002178, PLACE1000986, PLACE1001114, PLACE1001229, PLACE1001788, PLACE1003438, PLACE1003460, PLACE1003644, PLACE1004028, PLACE1004199, PLACE1004519, PLACE1005601, PLACE1005669, PLACE1005768, PLACE1006515, PLACE1006786, PLACE1007040, PLACE1007077, PLACE1007591, PLACE1007971, PLACE1008984, PLACE1009735, PLACE2000219, PLACE4000455, THYRO1000846, THYRO1000999, THYRO1001063, THYRO1001128, THYRO1001471, THYRO1001495, THYRO1001608, THYRO1001803, Y79AA1000127, Y79AA1000750, Y79AA1001592, Y79AA1001863,

[0052] In the 437 clones categorized into secretory and/or membrane proteins by using their full-length sequences, 410 clones were also predicted to encode proteins having functions of secretory and/or membrane proteins by using their partial nucleotide sequences. In the 146 clones categorized into glycoprotein-associated proteins by using their full-length sequences, 124 clones were also predicted to encode proteins having functions of glycoprotein-associated proteins by using their partial nucleotide sequences. In the 57 clones categorized into signal transduction-associated proteins by using their full-length sequences, 46 clones were also predicted to encode proteins having functions of signal transduction-associated proteins by using their partial nucleotide sequences. In the 81 clones categorized into transcription-associated proteins by using their full-length sequences, 57 clones were also predicted to encode proteins having functions of transcription-associated proteins by using their partial nucleotide sequences. In the 85 clones categorized into disease-associated proteins by using their full-length sequences, 6 clones were also predicted to encode proteins having functions of disease-associated proteins by using their partial nucleotide sequences. The number of clones, which were predicted to encode disease-associated proteins based on the full-length nucleotide sequences, is much greater than that predicted based on the partial sequences. The reason is that the full-length sequences were categorized by using the data found in the OMIM database into the category of disease-associated proteins.

[0053] In some cases, the predicted functions based on the partial sequences are different from those based on the full-length sequences. The reason is that a protein does not always belong solely to a single category of the above-described functional categories, and therefore, it is possible for the protein to belong to both of the predicted functional categories. Besides, additional functions can be found for the clones classified into these functional categories by further analyses.

[0054] The following list shows the cDNA clones predicted and selected on the basis of the partial sequences (5' sequences) as cDNAs encoding secretory and/or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins, or disease-associated proteins.

[0055] The clones that are selected by the score in the ATGpr and by the PSORT for the existence of a signal sequence can be expected to encode a secretory or membrane protein since they are predicted to possess the secretion

signal or a transmembrane region. The clones that are selected by the score in the ATGpr and by the PSORT for the existence of a signal sequence are listed below (254 clones).

HEMBA1000300 HEMBA1000713 HEMBA1000907
HEMBA1000962 HEMBA1001272 HEMBA1001297
HEMBA1002164 HEMBA1002239 HEMBA1002420
HEMBA1002421 HEMBA1003101 HEMBA1003294
HEMBA1003399 HEMBA1003602 HEMBA1003732
HEMBA1004110 HEMBA1004797 HEMBA1005430
HEMBA1006016 HEMBA1006171 HEMBA1006311
HEMBA1006335 HEMBA1006357 HEMBA1006572
HEMBA1006658 HEMBA1006707 HEMBA1006902
HEMBA1006960 HEMBA1007013 HEMBB1000276
HEMBB1000447 HEMBB1000567 HEMBB1000642
HEMBB1000905 HEMBB1001200 HEMBB1001407
HEMBB1001530 HEMBB1001547 HEMBB1001978
HEMBB1002162 HEMBB1002228 HEMBB1002245
HEMBB1002427 HEMBB1002465 HEMBB1002663
HEMBB1002693 MAMMA1000046 MAMMA1000102
MAMMA1000118 MAMMA1000141 MAMMA1000449
MAMMA1000457 MAMMA1000591 MAMMA1000652
MAMMA1000681 MAMMA1000986 MAMMA1000994
MAMMA1001043 MAMMA1001141 MAMMA1001284
MAMMA1001310 MAMMA1001344 MAMMA1001893
MAMMA1001901 MAMMA1001957 MAMMA1002070
MAMMA1002087 MAMMA1002165 MAMMA1002205
MAMMA1002224 MAMMA1002633 NT2RM2000241
NT2RM2000306 NT2RM2000410 NT2RM2000514
NT2RM2001643 NT2RM2001941 NT2RM4000115
NT2RM4000997 NT2RM4001321 NT2RM4001325
NT2RM4001768 NT2RP1000050 NT2RP1000448
NT2RP1000903 NT2RP1001563 NT2RP2000479
NT2RP2001495 NT2RP2001915 NT2RP2001948
NT2RP2002015 NT2RP2002063 NT2RP2002304
NT2RP2002674 NT2RP2002721 NT2RP2003383
NT2RP2003469 NT2RP2003593 NT2RP2003599
NT2RP2003655 NT2RP2003664 NT2RP2004179
NT2RP2004447 NT2RP2004495 NT2RP2004524
NT2RP2004556 NT2RP2004837 NT2RP2005027
NT2RP2005463 NT2RP2005514 NT2RP2005887
NT2RP2006042 NT2RP2006269 NT2RP3000169
NT2RP3000460 NT2RP3000481 NT2RP3000645
NT2RP3000789 NT2RP3000818 NT2RP3001012
NT2RP3001044 NT2RP3001195 NT2RP3001560
NT2RP3001685 NT2RP3001858 NT2RP3002160
NT2RP3002281 NT2RP3002721 N12RP3002836
NT2RP3002958 NT2RP3003076 NT2RP3003354
NT2RP3003469 NT2RP3003535 NT2RP3003559
NT2RP3003963 NT2RP3004000 NT2RP3004083
NT2RP3004133 NT2RP3004309 NT2RP3004321
NT2RP3004355 NT2RP3004374 NT2RP4001001
NT2RP4001879 NT2RP4002451 NT2RP4002715
OVARC1000208 OVARC1000298 OVARC1000439
OVARC1000775 OVARC1000811 OVARC1000853
OVARC1001222 OVARC1001727 OVARC1001807
OVARC1001833 PLACE1000231 PLACE1000560
PLACE1000740 PLACE1000912 PLACE1000914
PLACE1000927 PLACE1000986 PLACE1001100

PLACE1001183 PLACE1001229 PLACE1001407
PLACE1001536 PLACE1001788 PLACE1002080
PLACE1002095 PLACE1002374 PLACE1002518
PLACE1003407 PLACE1003428 PLACE1003460
PLACE1003839 PLACE1003845 PLACE1004028
PLACE1004199 PLACE1004282 PLACE1004305
PLACE1004482 PLACE1004637 PLACE1005005
PLACE1005250 PLACE1005383 PLACE1005410
PLACE1005544 PLACE1005569 PLACE1005601
PLACE1005660 PLACE1005669 PLACE1005725
PLACE1005768 PLACE1005927 PLACE1006079
PLACE1006093 PLACE1006219 PLACE1006277
PLACE1006443 PLACE1006786 PLACE1006809
PLACE1007040 PLACE1007096 PLACE1007296
PLACE1007626 PLACE1007971 PLACE1008469
PLACE1008984 PLACE1008985 PLACE1009067
PLACE1009196 PLACE1009527 PLACE1009982
PLACE1010251 PLACE1011236 PLACE2000219
PLACE4000455 SKNMC1000004 SKNMC1000014
THYRO1000036 THYRO1000099 THYRO1000196
THYRO1000795 THYRO1000999 THYRO1001237
THYRO1001327 THYRO1001478 THYRO1001495
THYRO1001523 THYRO1001702 THYRO1001725
Y79AA1000226 Y79AA1000270 Y79AA1000426
Y79AA1000521 Y79AA1000776 Y79AA1000959
Y79AA1001013 Y79AA1001056 Y79AA1001264
Y79AA1001328 Y79AA1001427 Y79AA1001430
Y79AA1001530 Y79AA1001592 Y79AA1001793
Y79AA1001795 Y79M1001803 Y79AA1001863
Y79AA1002022 Y79AA1002373

[0056] In the example mentioned below, the 254 clones as described above were categorized into three groups according to their maximal value in the ATGpr and the result in the PSORT, which are shown in Table 7-10, 11, 12 (246 clones), and Table 13, 14, 15 (8 clones). In the tables, the name of clone, indicate the name of the clone that was selected by the ATGpr and the PSORT; the name of sequence indicates the name of the 5'-end sequence of the clone on the left; the maximal ATGpr score indicates the maximal ATGpr1 score of the 5'-end sequence shown on the left; and signal indicates the presence of the signal sequence according to the prediction by the PSORT. In addition, the representative sequence is the sequence that has the longest sequence among the cluster in which the 5'-end sequence on the left was included. The maximal ATGpr score and signal on the right indicate the maximal ATGpr1 score of the representative sequence, and the presence of a signal sequence in the representative sequence according to the prediction by the PSORT, respectively. The 170 clones shown in Table 7-10, having the maximal score in the ATGpr1 higher than 0.5, and predicted to possess a signal sequence by the PSORT, are very likely to be full-length and encode a secretory or membrane protein. The 35 clones in Table 11, which have the maximal score in the ATGpr1 0.3 or higher and less than 0.5, and predicted to have a signal sequence, are also as well. And, the 41 clones in Table 12, having the maximal score in the ATGpr1 0 or higher and less than 0.3, and predicted to have a signal sequence, are likely to be full-length and encode a secretory or membrane protein.

[0057] The 8 clones in Table 13 (4 clones), Table 14 (2 clones), and Table 15 (2 clones) have the maximal score in the ATGpr1 0.5 or higher, 0.3 or higher and less than 0.5, and 0 or higher and less than 0.3, respectively, and are predicted to have no signal sequence by the PSORT. However, these clones contain a region that is recognized by the PSORT to be a signal sequence within the representative sequence composing the same cluster. Thus, the clones were judged as a full-length clone which encodes a membrane protein, especially.

[0058] The clones selected by the score in the ATGpr and by the keywords in the top hit data in the SwissProt are likely to encode a secretory or membrane protein, or proteins with functions associated to signal transduction, glycoprotein, transcription, and diseases according to the respective keywords. These 659 clones are shown below. Here, top hit data is defined to be data of known amino acid sequence which is identified to be the most homologous sequence in homology search using the SwissProt.

BNGH41000020 BNGH41000087 BNGH41000091

HEMBA1000006 HEMBA1000121 HEMBN1000128
HEMBA1000275 HEMBA1000349 HEMBA1000443
HEMBA1000462 HEMBA1000477 HEMBA1000590
HEMBA1000634 HEMBA1000671 HEMBA1000732
HEMBA1000745 HEMBA1000835 HEMBA1000875
HEMBA1000907 HEMBA1000940 HEMBA1001184
HEMBA1001221 HEMBA1001228 HEMBA1001296
HEMBA1001390 HEMBA1001563 HEMBA1001621
HEMBA1001878 HEMBA1001886 HEMBA1002048
HEMBA1002131 HEMBA1002163 HEMBA1002164
HEMBA1002167 HEMBA1002178 HEMBA1002195
HEMBA1002227 HEMBA1002316 HEMBA1002421
HEMBA1002524 HEMBA1002551 HEMBA1002767
HEMBA1002985 HEMBA1002992 HEMBA1003047
HEMBA1003072 HEMBA1003101 HEMBA1003120
HEMBA1003230 HEMBA1003315 HEMBA1003392
HEMBA1003487 HEMBA1003497 HEMBA1003530
HEMBA1003945 HEMBA1004007 HEMBA1004067
HEMBA1004085 HEMBA1004250 HEMBA1004391
HEMBA1004444 HEMBA1004454 HEMBA1004505
HEMBA1004785 HEMBA1004797 HEMBA1004952
HEMBA1004971 HEMBA1004982 HEMBA1005070
HEMBA1005084 HEMBA1005145 HEMBA1005230
HEMBA1005246 HEMBA1005267 HEMBA1005337
HEMBA1005449 HEMBA1005489 HEMBA1005522
HEMBA1005545 HEMBA1005698 HEMBA1005913
HEMBA1005929 HEMBA1005945 HEMBA1006276
HEMBA1006299 HEMBA1006335 HEMBA1006430
HEMBA1006482 HEMBA1006517 HEMBA1006544
HEMBA1006572 HEMBA1006707 HEMBA1006724
HEMBA1006749 HEMBA1006770 HEMBA1006902
HEMBA1006912 HEMBA1006916 HEMBA1007013
HEMBA1007057 HEMBA1007063 HEMBA1007226
HEMBA1007241 HEMBA1007291 HEMBA1007332
HEMBB1000106 HEMBB1000309 HEMBB1000407
HEMBB1000447 HEMBB1000542 HEMBB1000567
HEMBB1000668 HEMBB1000679 HEMBB1000881
HEMBB1001026 HEMBB1001048 HEMBB1001200
HEMBB1001573 HEMBB1001847 HEMBB1001959
HEMBB1002039 HEMBB1002041 HEMBB1002051
HEMBB1002120 HEMBB1002302 HEMBB1002427
HEMBB1002661 MAMMA1000106 MAMMA1000204
MAMMA1000226 MAMMA1000403 MAMMA1000473
MAMMA1000496 MAMMA1000528 MAMMA1000591
MAMMA1000614 MAMMA1000681 MAMMA1000706
MAMMA1000788 MAMMA1000810 MAMMA1000814
MAMMA1000881 MAMMA1001043 MAMMA1001066
MAMMA1001094 MAMMA1001150 MAMMA1001237
MAMMA1001418 MAMMA1001532 MAMMA1001609
MAMMA1001615 MAMMA1001623 MAMMA1001634
MAMMA1001893 MAMMA1001957 MAMMA1001978
MAMMA1002070 MAMMA1002080 MAMMA1002091
MAMMA1002095 MAMMA1002128 MAMMA1002142
MAMMA1002165 MAMMA1002234 MAMMA1002586
MAMMA1002633 MAMMA1003126 NT2RM1000407
NT2RM1000462 NT2RM1000542 NT2RM1000580
NT2RM1000789 NT2RM1000855 NT2RM1000858
NT2RM1000899 NT2RM2000410 NT2RM2000423

NT2RM2000497 NT2RM2000565 NT2RM2000582
NT2RM2000589 NT2RM2000622 NT2RM2000632
NT2RM2000773 NT2RM2001126 NT2RM2001558
NT2RM2001626 NT2RM2001738 NT2RM2001767
NT2RM2001792 NT2RM2001818 NT2RM2001902
NT2RM2001939 NT2RM2001941 NT2RM4000100
NT2RM4000198 NT2RM4000284 NT2RM4000295
NT2RM4000326 NT2RM4000417 NT2RM4000444
NT2RM4000587 NT2RM4000593 NT2RM4000648
NT2RM4000761 NT2RM4000965 NT2RM4001377
NT2RM4001735 NT2RM4001843 NT2RM4002352
NT2RP1000002 NT2RP1000050 NT2RP1000181
NT2RP1000239 NT2RP1000261 NT2RP1000271
NT2RP1000300 NT2RP1000325 NT2RP1000465
NT2RP1000468 NT2RP1000551 NT2RP1000579
NT2RP1000613 NT2RP1000679 NT2RP1000740
NT2RP1000981 NT2RP1001004 NT2RP1001020
NT2RP1001031 NT2RP2000092 NT2RP2000178
NT2RP2000240 NT2RP2000394 NT2RP2000447
NT2RP2000514 NT2RP2000533 NT2RP2000610
NT2RP2000616 NT2RP2000649 NT2RP2000663
NT2RP2000694 NT2RP2000712 NT2RP2000739
NT2RP2000818 NT2RP2000903 NT2RP2001200
NT2RP2001223 NT2RP2001276 NT2RP2001388
NT2RP2001469 NT2RP2001480 NT2RP2001495
NT2RP2001514 NT2RP2001529 NT2RP2001538
NT2RP2001562 NT2RP2001662 NT2RP2001755
NT2RP2001769 NT2RP2001817 NT2RP2001878
NT2RP2001903 NT2RP2001921 NT2RP2001948
NT2RP2001956 NT2RP2002063 NT2RP2002188
NT2RP2002232 NT2RP2002304 NT2RP2002409
NT2RP2002510 NT2RP2002527 NT2RP2002533
NT2RP2002564 NT2RP2002824 NT2RP2002942
NT2RP2002974 NT2RP2002976 NT2RP2003042
NT2RP2003138 NT2RP2003179 NT2RP2003210
NT2RP2003302 NT2RP2003369 NT2RP2003390
NT2RP2003469 NT2RP2003545 NT2RP2003593
NT2RP2003655 NT2RP2003664 NT2RP2003931
NT2RP2003940 NT2RP2003950 NT2RP2004069
NT2RP2004108 NT2RP2004141 NT2RP2004205
NT2RP2004447 NT2RP2004606 NT2RP2004648
NT2RP2004670 NT2RP2004794 NT2RP2004847
NT2RP2005069 NT2RP2005163 NT2RP2005181
NT2RP2005247 NT2RP2005378 NT2RP2005391
NT2RP2005425 NT2RP2005535 NT2RP2005541
NT2RP2005597 NT2RP2005632 NT2RP2005666
NT2RP2005774 NT2RP2005878 NT2RP2005883
NT2RP2005941 NT2RP2005994 NT2RP2006004
NT2RP2006042 NT2RP2006092 NT2RP2006099
NT2RP2006134 NT2RP2006269 NT2RP2006512
NT2RP3000011 NT2RP3000022 NT2RP3000059
NT2RP3000063 NT2RP3000125 NT2RP3000148
NT2RP3000171 NT2RP3000172 NT2RP3000201
NT2RP3000232 NT2RP3000304 NT2RP3000378
NT2RP3000427 NT2RP3000436 NT2RP3000444
NT2RP3000481 NT2RP3000616 NT2RP3000645
NT2RP3000652 NT2RP3000676 NT2RP3000677
NT2RP3000721 NT2RP3000820 NT2RP3000838

NT2RP3000871 NT2RP3000907 NT2RP3000921
NT2RP3001012 NT2RP3001061 NT2RP3001159
NT2RP3001170 NT2RP3001195 NT2RP3001240
NT2RP3001271 NT2RP3001322 NT2RP3001388
NT2RP3001542 NT2RP3001560 NT2RP3001592
NT2RP3001650 NT2RP3001738 NT2RP3001754
NT2RP3001976 NT2RP3002015 NT2RP3002160
NT2RP3002286 NT2RP3002311 NT2RP3002324
NT2RP3002342 NT2RP3002353 NT2RP3002409
NT2RP3002411 NT2RP3002448 NT2RP3002571
NT2RP3002664 NT2RP3002737 NT2RP3002738
NT2RP3002790 NT2RP3002836 NT2RP3002887
NT2RP3002900 NT2RP3002958 NT2RP3002983
NT2RP3003000 NT2RP3003076 NT2RP3003354
NT2RP3003448 NT2RP3003473 NT2RP3003527
NT2RP3003532 NT2RP3003614 NT2RP3003729
NT2RP3003849 NT2RP3003874 NT2RP3003939
NT2RP3004025 NT2RP3004067 NT2RP3004075
NT2RP3004090 NT2RP3004119 NT2RP3004130
NT2RP3004133 NT2RP3004202 NT2RP3004294
NT2RP3004309 NT2RP3004345 NT2RP3004406
NT2RP3004481 NT2RP3004552 NT2RP3004557
NT2RP3004625 NT2RP3004640 NT2RP3004647
NT2RP4000108 NT2RP4000634 NT2RP4000962
NT2RP4001009 NT2RP4001467 NT2RP4001877
NT2RP4001879 NT2RP4002187 NT2RP4002451
NT2RP4002750 OVARC1000003 OVARC1000090
OVARC1000105 OVARC1000137 OVARC1000255
OVARC1000275 OVARC1000307 OVARC1000313
OVARC1000331 OVARC1000410 OVARC1000439
OVARC1000467 OVARC1000529 OVARC1000553
OVARC1000873 OVARC1000916 OVARC1000956
OVARC1000995 OVARC1001030 OVARC1001049
OVARC1001086 0VAPC1001132 OVARC1001163
OVARC1001222 OVARC1001260 OVARC1001336
OVARC1001338 OVARC1001569 OVARC1001570
OVARC1001596 OVARC1001607 OVARC1001725
OVARC1001952 OVARC1001991 OVARC1002058
OVARC1002178 PLACE1000033 PLACE1000258
PLACE1000442 PLACE1000740 PLACE1000907
PLACE1001016 PLACE1001114 PLACE1001123
PLACE1001231 PLACE1001340 PLACE1001401
PLACE1001407 PLACE1001464 PLACE1001500
PLACE1001516 PLACE1001564 PLACE1001655
PLACE1001795 PLACE1001836 PLACE1001918
PLACE1001949 PLACE1002080 PLACE1002095
PLACE1002153 PLACE1002329 PLACE1002355
PLACE1002374 PLACE1002547 PLACE1002726
PLACE1002905 PLACE1002911 PLACE1002967
PLACE1003135 PLACE1003163 PLACE1003428
PLACE1003438 PLACE1003460 PLACE1003529
PLACE1003573 PLACE1003598 PLACE1003644
PLACE1003737 PLACE1003772 PLACE1003852
PLACE1004078 PLACE1004166 PLACE1004168
PLACE1004279 PLACE1004441 PLACE1004450
PLACE1004482 PLACE1004492 PLACE1004519
PLACE1004520 PLACE1004630 PLACE1004648
PLACE1004816 PLACE1004887 PLACE1005003

PLACE1005031 PLACE1005239 PLACE1005383
PLACE1005426 PLACE1005519 PLACE1005539
PLACE1005544 PLACE1005569 PLACE1005682
PLACE1005736 PLACE1005745 PLACE1005815
PLACE1005878 PLACE1005927 PLACE1006071
PLACE1006073 PLACE1006208 PLACE1006277
PLACE1006290 PLACE1006443 PLACE1006515
PLACE1006716 PLACE1006959 PLACE1007028
PLACE1007077 PLACE1007081 PLACE1007096
PLACE1007296 PLACE1007591 PLACE1007702
PLACE1007845 PLACE1007881 PLACE1008282
PLACE1008297 PLACE1008359 PLACE1008469
PLACE1008549 PLACE1008657 PLACE1008716
PLACE1008744 PLACE1008984 PLACE1008985
PLACE1009279 PLACE1009527 PLACE1009546
PLACE1009600 PLACE1009735 PLACE1010011
PLACE1010078 PLACE1010081 PLACE1010251
PLACE1010445 PLACE1010713 PLACE1010784
PLACE1010827 PLACE1010968 PLACE1011045
PLACE1011116 PLACE1011181 PLACE1011236
PLACE1011364 PLACE1011407 PLACE1011516
PLACE1011708 PLACE1011824 PLACE1011978
PLACE2000118 PLACE3000181 PLACE3000213
PLACE4000354 SKNMC1000014 SKNMC1000082
THYRO1000061 THYRO1000196 THYRO1000400
THYRO1000580 THYRO1000584 THYRO1000678
THYRO1000776 THYRO1000795 THYRO1000846
THYRO1000866 THYRO1000956 THYRO1000964
THYRO1001063 THYRO1001071 THYRO1001102
THYRO1001113 THYRO1001128 THYRO1001205
THYRO1001242 THYRO1001266 THYRO1001456
THYRO1001457 THYRO1001471 THYRO1001478
THYRO1001529 THYRO1001593 THYRO1001608
THYRO1001641 THYRO1001700 THYRO1001702
THYRO1001770 THYRO1001803 Y79AA1000030
Y79AA1000127 Y79AA1000207 Y79AA1000270
Y79AA1000426 Y79AA1000750 Y79AA1000777
Y79AA1000876 Y79AA1000888 Y79AA1000967
Y79AA1001062 Y79AA1001090 Y79AA1001212
Y79AA1001272 Y79AA1001426 Y79AA1001523
Y79AA1001727 Y79AA1001787 Y79AA1001799
Y79AA1001803 Y79AA1001863 Y79AA1002058
Y79AA1002121 Y79AA1002129 Y79AA1002213
Y79AA1002334 Y79AA1002376 Y79AA1002378
Y79AA1002381 NT2RP2006580

[0059] Among the clones, the following 83 clones are identical to the clones selected by the score in the ATGpr and the prediction by the PSORT for the existence of a signal sequence.

HEMBA1000907 NT2RM2000410 PLACE1000740
HEMBA1002164 NT2RM2001941 PLACE1001407
HEMBA1002421 NT2RP1000050 PLACE1002080
HEMBA1003101 NT2RP2001495 PLACE1002095
HEMBA1004797 NT2RP2001948 PLACE1002374
HEMBA1006335 NT2RP2002063 PLACE1003428
HEMBA1006572 NT2RP2002304 PLACE1003460
HEMBA1006707 NT2RP2003469 PLACE1004482
HEMBA1006902 NT2RP2003593 PLACE1005383

HEMBA1007013 NT2RP2003655 PLACE1005544
HEMBB1000447 NT2RP2003664 PLACE1005569
HEMBB1000567 NT2RP2004447 PLACE1005927
HEMBB1001200 NT2RP2006042 PLACE1006277
HEMBB1002427 NT2RP2006269 PLACE1006443
MAMMA1000591 NT2RP3000481 PLACE1007096
MAMMA1000681 NT2RP3000645 PLACE1007296
MAMMA1001043 NT2RP3001012 PLACE1008469
MAMMA1001893 NT2RP3001195 PLACE1008984
MAMMA1001957 NT2RP3001560 PLACE1008985
MAMMA1002070 NT2RP3002160 PLACE1009527
MAMMA1002165 NT2RP3002836 PLACE1010251
MAMMA1002633 NT2RP3002958 PLACE1011236
NT2RP3003076 SKNMC1000014
NT2RP3003354 THYPO1000196
NT2RP3004133 THYRO1000795
NT2RP3004309 THYRO1001478
NT2RP4001879 THYRO1001702
NT2RP4002451 Y79AA1000270
OVARC1000439 Y79AA1000426
OVARC1001222 Y79AA1001803
Y79AA1001863

[0060] The 446 clones in Table 16, 17, 18, 19, and 20, and NT2RP2006580 are predicted to encode a secretory or membrane protein. Among them, 77 clones were identical to the clones selected by the score in the ATGpr and the prediction by the PSORT for the existence of a signal sequence (overlapping with any of the 254 clones listed in Table 7-15). Besides, many clones were turned out to be identical to the clones selected as a protein associated with a glycoprotein. Also, there were clones identical to those selected as a protein associated with a disease.

[0061] The 243 clones in Table 21 are predicted to encode a glycoprotein. Among them, 53 clones were identical to those selected by the score in the ATGpr and the prediction by the PSORT for the existence of a signal sequence. And, many clones were turned out to be identical to the clones selected as a secretory or membrane protein. Moreover, there were clones identical to those selected as a protein associated with a disease.

[0062] The 51 clones in Table 22 are predicted to encode a protein associated to signal transduction.

[0063] The 130 clones in Table 23 are predicted to encode a protein associated to transcription.

[0064] The 17 clones in Table 24 are predicted to encode a protein associated with diseases.

[0065] In these clones, 532 clones have the maximal ATGpr1 score of 0.5 or higher (Table 25). 60 clones have the maximal ATGpr1 score of 0.3 or higher and less than 0.5 (Table 26 and NT2RP2006580). And 67 clones were with the maximal ATGpr1 score of 0 or higher and less than 0.3 (Table 27).

[0066] 532 clones shown in Table 25, each having the maximal score in the ATGpr1 0.5 or higher, are very likely to be full-length and encode a secretory or membrane protein, or proteins associated to signal transduction, glycoprotein, transcription, or diseases. 59 clones in Table 26 and NT2RP2006580, which have the maximal score in the ATGpr1 0.3 or higher and less than 0.5, are likely to be full-length and encode a secretory or membrane protein, or proteins associated to signal transduction, glycoprotein, transcription, or diseases. 67 clones in Table 27, having the maximal score in the ATGpr1 0 or higher and less than 0.3, are still likely to be full-length and encode a secretory or membrane protein, or proteins associated to signal transduction, glycoprotein, transcription, or diseases.

[0067] This is the method for selecting the cDNA clones predicted to encode secretory and/or transmembrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins, or disease-associated proteins on the basis of the partial sequences (5' sequences).

[0068] The polynucleotide of the present invention encodes an amino acid sequence of a functional protein such as a secretory or membrane protein, or a protein associated to signal transduction, glycoprotein, transcription, or diseases. Since the protein has the complete amino acid sequence, it is possible to analyze its biological activity by expressing the protein as a recombinant protein using an appropriate expression system, or by raising and using an antibody which specifically recognizes it.

[0069] It is possible to analyze the biological activity of a secretory protein or a membrane protein, or proteins associated to signal transduction, glycoprotein, or transcription, based on the methods in "Gene Transcription" (Hames B. D., and Higgins S.J. edit, (1993)), "Glycobiology" (Fukuda M., and Kobata A. edit, (1993)), "Growth Factors" (McKay I., and Leigh I. edit, (1993)), "Extracellular Matrix" (Haralson M.A., and Hassell J.R. edit, (1995), "Transcription Factors" (Latchman D.S. edit, (1993)), "Signal Transduction" (Milligans G. edit, (1992)), featured in "The Practical Approach

Series" (IRL PRESS), or "Signal Transduction Protocols" (Kendall D.A., and Hill S.J. edit, (1995), "Glycoprotein Analysis in Biomedicine" (Hounsell E.F. edit, (1993)), featured in "Method in Molecular Biology" (Humana Press).

[0070] As to a protein associated with a disease, it is possible to perform a functional analysis as described above, but also possible to analyze correlation between the expression or the activity of the protein and a certain disease by using a specific antibody that recognizes the protein. Alternatively, it is possible to utilize the database Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/Omim/), which is a database of human genes and diseases, to analyze the protein. New information is constantly being deposited in the OMIM database. Therefore, it is possible for one skilled in the art to find a new relationship between a particular disease and a gene of the present invention in the updated database.

[0071] Proteins associated with diseases are useful in drug development as they can be utilized as a diagnostic marker, a drug that regulates the level of their expression and activities, or a target of gene therapy. Also, as for a secretory protein, membrane protein, or proteins associated with signal transduction, glycoprotein, or transcription, search of the OMIM with the keywords mentioned below revealed that the proteins are associated with many diseases. Also, relationship between a proteins associated to signal transduction or transcription and diseases is reported in "Transcription Factor Research-1999" (Fujii, Tamura, Morohashi, Kageyama, and Satake edit, (1999) Jikken-Igaku Zoukan, Vol.17, No.3), and "Gene Medicine" ((1999) Vol.3, No.2). Thus, not only a protein associated with diseases, but also a secretory protein, membrane protein, or protein associated with signal transduction, glycoprotein, or transcription is involved in diseases, suggesting these proteins also are very important as a target in medical industry.

[0072] Keywords used in the search of the OMIM

(1) secretion protein
(2) membrane protein
(3) channel
(4) extracellular matrix
(5) receptor
(6) glycoprotein
(7) protein kinase
(8) calmodulin kinase
(9) transcription factor

[0073] Shown in the search result are only the accession numbers in the OMIM. Using the number, data showing the relationship between a disease and a gene or protein can be seen. The OMIM data has been renewed everyday.

1) Secretion protein
268 entries found, searching for "secretion protein"
104760, 176860, 160900, 107400, 118910, 139320, 603850, 147572, 176880, 600946, 603215, 157147, 600174, 151675, 170280, 179512, 179513, 138120, 179509, 246700, 179510, 600626, 179511, 600998, 109270, 601489, 154545, 179490, 185860, 603216, 122559, 601746, 147290, 602672, 146770, 603062, 179508, 131230, 601591, 602421, 139250, 167805, 167770, 600041, 600564, 118825, 601146, 300090, 600753, 601652, 600759, 600768, 602434, 182590, 603166, 308230, 602534, 603489, 107470, 150390, 104610, 173120, 158106, 143890, 306900, 308700, 134797, 137350, 227500, 176300, 107730, 600760, 138079, 120180, 120160, 120150, 124092, 138160, 101000, 227600, 600509, 601199, 142410, 104311, 193400, 201910, 107300, 122560, 272800, 217000, 590050, 147670, 133170, 176730, 300300, 134370, 274600, 120140, 162151, 158070,
152790, 120120, 106100, 300200, 192340, 190160, 138040, 147470, 147620, 173350, 147380, 152200, 152760, 157145, 153450, 264080, 113811, 600937, 600840, 188545, 202110, 600514, 186590, 603372, 136435, 137241, 252800, 214500, 207750, 138850, 139191, 142640, 138130, 189907, 603692, 600633, 603355, 107270, 600377, 147892, 232200, 600281, 232800, 602358, 137035, 601771, 601769, 253200, 601933, 118444, 600270, 120700, 600945, 603732, 147660, 600761, 172400, 600823, 600877, 130080, 171060, 107740, 307800, 602843, 130660, 152780, 124020, 601124, 601340, 601604, 601610, 171050, 312060, 232700, 300159, 142703, 600734, 125255, 168450, 123812, 188540, 147940, 188450, 600839, 182452, 188400, 182280, 176760, 263200, 600264, 188826, 252650, 601185, 162641, 137216, 601398, 601538, 118888, 118445, 601745,
190180, 601922, 182098, 602008, 147440, 602384, 600031, 109160, 602663, 151670, 602682, 602730, 602779, 146880, 603061, 142704, 603140, 106150, 600732, 153620, 603318, 139392, 600042, 102200, 603493, 182100, 264300, 603795, 184600

2) Membrane protein
1017 entries found, searching for "membrane protein"
130500, 305360, 153330, 173610, 170995, 109270, 170993, 309060, 120920, 602333, 133740, 133710, 602690,

133730, 159430, 600897, 133090, 601178, 602413, 602003, 109280, 603237, 602173, 107776, 602334, 125305, 602335, 182879, 154045, 309845, 600594, 603718, 603241, 603214, 603657, 603177, 600182, 601476, 602879, 136950, 600723, 601114, 185880, 185881, 300096, 602257, 160900, 177070, 603062, 603344, 602977, 310200, 600959, 300100, 186945, 600039, 600267, 128240, 182900, 601097, 136430, 600946, 602534, 601047, 143450, 603141, 603700, 600579, 256540, 159440, 602414, 600403, 602048, 188860, 137290, 158343, 184756, 602910, 603179, 600279, 108733, 107770, 173335, 602625, 154050, 219800, 603850, 601028, 600447, 104225, 186946, 601767, 603143, 121015, 603215, 227400, 603735, 600179, 602421, 180721,

176801, 176860, 600753, 603142, 176790, 600266, 601239, 115501, 143890, 121014, 121011, 125950, 603534, 304040, 601134, 600754, 601510, 601595, 190315, 300172, 602216, 602261, 602262, 602461, 131560, 179514, 179512, 176981, 142461, 139310, 312080, 176640, 128239, 185470, 310300, 601403, 601757, 273800, 151460, 176943, 104311, 168468, 120130, 602887, 600164, 601531, 601832, 104775, 600040, 603583, 176894, 602631, 166945, 182180, 120620, 141180, 601014, 139150, 182860, 177061, 600174, 180069, 191275, 104760, 601693, 300017, 603518, 601009, 134651, 601107, 103868, 600168, 136425, 603531, 603291, 600917, 603216, 102720, 300118, 179590, 135630, 602285, 107450, 602296, 303630, 176878, 120090, 600322, 138160, 601212, 603293, 131230, 112205, 600763, 600718, 300187, 170715, 601966, 300051, 602474,

120070, 600691, 600855, 182309, 602101, 602857, 194355, 162230, 600874, 113730, 155550, 602701, 306400, 601789, 231200, 107271, 175100, 182870, 305100, 301000, 601313, 157147, 147670, 139200, 603593, 157655, 600934, 155970, 602049, 155960, 155760, 118990, 135620, 308230, 602694, 162060, 300023, 160993, 153619, 153432, 120131, 603823, 603167, 601023, 600816, 165040, 601681, 166490, 300112, 120190, 300145, 163970, 600772, 602926, 602933, 602202, 400015, 151510, 600759, 602672, 602654, 603821, 116952, 151430, 602632, 155975, 602217, 150370, 600752, 601179, 600932, 603048, 603234, 601805, 603822, 603869, 601717, 601181, 313440, 139130, 107777, 109190, 603452, 191163, 191164, 602370, 176877, 103195, 600523, 191328, 601275, 204200, 602426, 603820, 600551, 600695, 600552, 600553, 602306, 601523,

602507, 602299, 600583, 114070, 600632, 603498, 185430, 600587, 235200, 173470, 603199, 601633, 602500, 208900, 180297, 156225, 516020, 190195, 141900, 102680, 193300, 101000, 193400, 300011, 107400, 257220, 107741, 180380, 203200, 111700, 600024, 304800, 600065, 110750, 179605, 113705, 601638, 222900, 120120, 602509, 602469, 600930, 601383, 176261, 602574, 602997, 311770, 131550, 603616, 308700, 603372, 256100, 224100, 276903, 305900, 516000, 131195, 314555, 601567, 603866, 306900, 103390, 186720, 173850, 601050, 602505, 186590, 246530, 602689, 194380, 300041, 162643, 152790, 120150, 600682, 600106, 272750, 188040, 602382, 601497, 113811, 182138, 212138, 601309, 109690, 114760, 176805, 601253, 123900, 602581, 189980, 191190, 110700, 600163, 137167, 600580, 601610, 190000, 123825, 603491,

600135, 186591, 173910, 138140, 107266, 120950, 601081, 603690, 244400, 312700, 171060, 601199, 601758, 170500, 277900, 601997, 314850, 601880, 603009, 120220, 603126, 164920, 602934, 164730, 163890, 603434, 107269, 602909, 600877, 256550, 164761, 602872, 120110, 126150, 158070, 266200, 223360, 250800, 269920, 252650, 603355, 154582, 138190, 300035, 602640, 227650, 158120, 153700, 182380, 155740, 204500, 603401, 601975, 300135, 136350, 602924, 300167, 185050, 176100, 300189, 151525, 300200, 165180, 230800, 602158, 602676, 603411, 193245, 120325, 601848, 192500, 603102, 147795, 245900, 137060, 147557, 120650, 602377, 307800, 120930, 308100, 142800, 191092, 232300, 173510, 602225, 180470, 190930, 186357, 134638, 600544, 601373, 600509, 600359, 603784, 600395, 600653, 603754, 601597, 601066,

600185, 601295, 600978, 205400, 603274, 600418, 600839, 516050, 601691, 601007, 600650, 600308, 603261, 601193, 600004, 600017, 516040, 253800, 276901, 600019, 257200, 108780, 300037, 300104, 300126, 255125, 203300, 300191, 426000, 302060, 304700, 201475, 252010, 193210, 311030, 306250, 248600, 191740, 108360, 131244, 600423, 232200, 191305, 231680, 103320, 190180, 600493, 111200, 226200, 312600, 600170, 111680, 186910, 203100, 600536, 600238, 186830, 186760, 186745, 186711, 106180, 111203, 103180, 182530, 182160, 600644, 307030, 192321, 600667, 125647, 179080, 114207, 114860, 176000, 116930, 600748, 173515, 173325, 600377, 171760, 171050, 118425, 170260, 191315, 600798, 600821, 600823, 600444, 600840, 159465, 600857, 158380, 600867, 154360, 152427, 150330, 110900, 147840, 147360, 147280,

146880, 312610, 120940, 142871, 142790, 600937, 142600, 134390, 111250, 600979, 600997, 142460, 186845, 134635, 601017, 139191, 139090, 138850, 601040, 138720, 122561, 131100, 123610, 217070, 100500, 603377, 602354, 603302, 603207, 603086, 602188, 602095, 603867, 603842, 603798, 602602, 601194, 602607, 603713, 603681, 601252, 603648, 603646, 603644, 601282, 601284, 603667, 603712, 603594, 601872, 603425, 601843, 603263, 603208, 601411, 603201, 603189, 601463, 603164, 603152, 603087, 602874, 601492, 602893, 602057, 602859, 602746, 603879, 603510, 602458, 603380, 601581, 603765, 603283, 601599, 601733, 601852, 602316, 601615, 601617, 602184, 602894, 603005, 603030, 603861, 602835, 602136, 600153, 600074, 600046, 600023, 601625, 516006, 600018, 600016, 516002, 601590, 313475, 313470, 600244,

600528, 601611, 600282, 600327, 601568, 600368, 601730, 601535, 601745, 601929, 300169, 300150, 300132, 601533, 600385, 600464, 600424, 600429, 601756, 601488, 516005, 251100, 516004, 600918, 516003, 602192, 516001, 240500, 600465, 602241, 602243, 230200, 601485, 601478, 601416, 602297, 601459, 601839, 602314,

193065, 193001, 191306, 600504, 601020, 191191, 602372, 190181, 600534, 188380, 186854, 186360, 600530, 185250, 182331, 600535, 182305, 601296, 600582, 600732, 600734, 600742, 600782, 176802, 176266, 600769, 601883, 600864, 601901, 176260, 173490, 600910, 601905, 171890, 600916, 601987, 602679, 162651, 161555, 160994, 602714, 602715, 602724, 602736, 300007, 602783, 275630, 602836, 270200, 602871, 159460, 602876, 154540, 153900, 602890, 601153, 602190, 602905, 153634, 153337, 602914, 152310, 151690, 151625, 602935, 602974, 150325, 602992, 150320, 250790, 603006, 603007, 603008, 150292, 233690, 603046, 150210, 603061, 147940, 603063, 221770, 223100, 603097, 147880, 603118, 147730, 146928, 146630, 142622, 603149, 603150, 603151, 600923, 138981, 138590, 138330, 216950, 603192, 138297, 603202, 601002, 602343, 138230, 136131, 603217, 603220, 134660, 131390, 131235, 603242, 603243, 130130, 602345, 126455, 601123, 126064, 125240, 602359, 603312, 602380, 603318, 123890, 123836, 603356, 603361, 603366, 123830, 179610, 188060, 123620, 120980, 186355, 118510, 114835, 114217, 113810, 603499, 182310, 111740, 109610, 603548, 603564, 108740, 603598, 603613, 107273, 603626, 602518, 179410, 603647, 602515, 603652, 106195, 602573, 178990, 105210, 104615, 167055, 603717, 104614, 603728, 104210, 603749, 603750, 103850, 602608, 603787, 603788, 603796, 173445, 103220, 102910, 102681, 102670, 102642, 603833, 173391, 102576, 102575, 171833, 102573, 101800, 603875, 601108

3) Channel
272 entries found, searching for "channel"
176266, 600724, 170500, 182390, 123825, 114208, 114205, 601784, 114206, 600937, 114204, 603415, 600053, 114209, 114207, 600760, 118425, 601011, 192500, 176261, 600761, 176260, 600359, 600228, 600877, 602235, 300008, 182389, 182391, 601328, 601534, 600504, 602323, 601958, 602780, 602781, 601327, 601012, 600734, 603208, 182392, 603220, 603219, 603888, 600054, 602232, 601745, 603537, 602604, 603796, 302910, 602866, 601013, 602905, 602906, 600163, 152427, 180901, 600702, 600308, 602754, 107776, 602024, 314555, 601949, 600235, 602023, 176263, 600681, 176265, 193245, 603305, 176258, 602983, 601219, 601141, 176267, 602343, 602726, 138253, 176262, 600003, 600397, 602872, 138249, 600843, 600935, 600580, 600845, 602158, 602106, 176264, 300110, 176257, 602717, 603493, 176268, 600932, 602727, 138254, 603652, 300138, 602420, 600570, 600150, 603583, 602345, 603749, 601142, 176256, 600846, 138252, 602982, 603787, 602836, 603788, 602566, 603651, 602421, 100690, 107777, 100725, 100710, 600509, 603061, 154275, 304040, 154276, 180902, 121014, 602368, 139311, 601383, 108745, 601313, 601042, 600131, 186360, 600109, 600229, 600170, 603319, 601485, 118503, 180903, 602076, 124030, 601059, 601212, 601218, 147450, 600855, 600919, 601154, 601157, 171060, 600968, 182139, 131230, 121015, 600421, 113730, 249210, 310500, 600637, 125950, 118800, 156490, 602974, 104610, 121011, 602522, 118504, 300041, 160900, 601382, 602103, 600465, 602014, 600442, 601109, 602481, 277900, 254210, 138247, 164920, 170280, 171050, 128100, 173910, 600884, 123885, 602887, 600232, 180297, 137192, 600304, 138251, 603053, 300103, 603152, 603199, 118511, 118508, 138079, 600983, 182307, 603324, 305990, 603418, 114080, 232200, 600046, 600040, 602403, 603750, 603785, 104210, 600019, 600300, 182860, 603852, 603853, 603855, 516060

4) Extracellular matrix
167 entries found, searching for "extracellular matrix"
603479, 602201, 601418, 601548, 154870, 115437, 602285, 602262, 602261, 134797, 600754, 120361, 116935, 602263, 603320, 601807, 603321, 185250, 185261, 253700, 128239, 120324, 193300, 276901, 308700, 600514, 600261, 602109, 120140, 120150, 147557, 193400, 600536, 188826, 120180, 118661, 120320, 152200, 135821, 112260, 230740, 602090, 155760, 192975, 190182, 602108, 601463, 186745, 600900, 600985, 600758, 602369, 179590, 601211, 600065, 602178, 600262, 182888, 182889, 151510, 182120, 150325, 190181, 150370, 186355, 193065, 165070, 154705, 147559, 146650, 146640, 153619, 175100, 187380, 231050, 188060, 135820, 156790, 130660, 301870, 128240, 600076, 600119, 193210, 600215, 600245, 121010, 150240, 600309, 600491, 222600, 120328, 600564, 600596, 600616, 600700, 600742, 120325, 138297, 600930, 156225, 601028, 601050, 601105, 253800, 601284, 601313, 120280, 310200, 601492, 120250, 601587, 601636, 601652, 601692, 601728, 120220, 601915, 602048, 155120, 310300, 120210, 120165, 120120, 118940, 116930, 602264, 116806, 602366, 120470, 602415, 602428, 602453, 602505, 602574, 603005, 603196, 603221, 603319, 107269, 216550, 103320, 603489, 603551, 603767, 603799, 603842

5) Receptor (including membrane proteins, and also including transcription factors, since nuclear proteins were not excluded in the search)
1606 entries found, searching for "receptor"
600408, 176943, 107770, 601531, 143890, 313700, 162643, 202200, 147670, 191306, 182131, 192321, 138249, 190120, 600264, 162321, 603613, 603614, 602164, 138251, 182134, 138040, 152790, 602393, 133430, 601769, 304800, 147280, 168468, 147730, 155555, 191190, 109760, 122561, 136537, 602034, 147138, 187930, 312861,

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6) Glycoprotein

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7) Protein kinase (a member of signal transduction)
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122560, 602382, 103320, 603597, 603510, 232600, 133170, 603353, 603345, 603318, 603309, 230400, 139250, 603296, 603272, 114240, 147557, 232400, 139259, 602122, 230200, 164014, 248600, 601703, 194364, 150000, 602102, 601683, 158070, 602170, 602007, 601306, 248610, 601387, 161770, 132800, 164760, 601902, 601253, 173470, 602930, 603691, 165360, 123835, 603544, 147265, 107777, 602377, 600605, 602869, 601121, 602388, 301300, 590060, 601059, 168461, 142600, 314555, 142410, 170290, 602498, 190090, 311030, 142409, 190181, 600966, 308100, 600936, 171900, 190182, 172405, 102600, 603754, 600281, 172430, 138249, 300039, 603154, 602642, 300041, 602659, 192240, 603473, 136537, 603134, 182280, 603084, 125660, 189990, 133430, 603755, 603302, 600737, 300144, 305400, 188545, 600652, 189940, 600633, 603009,
181031, 182160, 148500, 602384, 600650, 602190, 171150, 173490, 164765, 147780, 600910, 601272, 147880, 125255, 120090, 173390, 602668, 600483, 602995, 602996, 180860, 142445, 116949, 602681, 603027, 182125, 600327, 600799, 164757, 230450, 602730, 600782, 164880, 232700, 116935, 602303, 603203, 164710, 600244, 600206, 263200, 300034, 601487, 600980, 600956, 601985, 600884, 601956, 191041, 601568, 601586, 155960, 602288, 176761, 113900, 600581, 516050, 190070, 164940, 600544, 107941, 312861, 602373, 123836, 106165, 103850, 274270, 601922, 602355, 147420, 311010, 163800, 600536, 602018, 307200, 603619, 603652, 193001, 193245, 603729, 603752, 118888, 603796, 305600, 603852, 603853, 603886

8) Calmodulin kinase (a member of signal transduction)
35 entries found, searching for "calmodulin binding"
300172, 114180, 302020, 139312, 602584, 602293, 600310, 603379, 114106, 602350, 114105, 114213, 138249, 153430, 177061, 182520, 102680, 600489, 601478, 306000, 600490, 600922, 601302, 601568, 168890, 164795, 163730, 602698, 602699, 602987, 102681, 603384

9) Transcription factor
717 entries found, searching for "transcription factor"
305371, 189963, 164177, 600297, 600298, 163260, 189907, 173110, 600733, 189903, 189972, 600438, 600281, 189962, 157670, 602272, 600609, 189968, 189971, 189889, 107580, 189908, 601748, 601542, 601632, 600610, 189969, 600480, 601760, 176310, 603022, 600519, 601750, 123803, 600520, 600494, 164176, 602460, 603246, 113725, 107773, 189904, 602228, 147141, 132890, 189964, 164175, 142410, 313650, 164011, 164014, 164005, 601714, 600492, 164012, 601878, 600673, 600635, 191523, 602191, 600490, 602149, 189967, 140580, 164343, 603256, 600727, 600729, 600728, 140581, 600571, 601511, 102582, 189906, 600660, 124097, 314310, 600860, 600662, 184756, 600777, 600013, 600172, 600489, 601425, 600786, 600502, 602406, 600743, 189965, 603257, 602751, 602542, 603148, 603107, 603789, 602318, 156845, 123811, 600425,
600540, 600695, 601622, 147574, 601601, 602407, 602150, 601538, 600663, 603306, 165170, 187040, 602444, 189902, 189973, 600659, 600661, 601010, 600788, 602617, 601602, 602053, 601742, 300039, 602438, 602976, 600744, 602543, 602479, 600481, 600473, 603739, 600426, 603738, 189901, 603677, 600427, 603255, 600607, 600379, 189909, 601679, 600787, 602160, 601043, 601397, 601044, 600366, 300025, 602575, 602669, 601804, 601801, 176312, 176311, 600746, 602480, 602944, 600967, 600912, 306700, 306900, 193400, 601206, 480000, 191160, 601861, 164008, 600475, 600773, 600772, 600774, 142409, 156490, 600589, 601490, 151385, 600599, 184757, 602955, 234000, 603433, 603349, 603198, 602294, 600390, 603628, 147620, 600211, 601787, 601863, 147470, 603795, 603734, 152760, 104155, 128990, 601729, 600197, 147370,
173490, 603423, 600822, 188595, 603243, 600573, 601689, 142765, 603181, 600879, 603731, 600288, 602295, 121360, 164874, 300019, 162095, 602355, 603258, 126090, 159540, 300070, 600555, 600664, 601874, 153245, 191191, 601126, 601512, 146733, 131550, 142385, 601796, 603406, 602959, 601734, 601732, 139191, 139139, 600633, 138971, 600006, 603170, 601488, 147576, 147680, 601498, 602630, 602643, 603364, 600914, 154040, 602746, 128992, 143089, 160900, 600140, 134934, 133510, 176860, 190180, 601150, 601175, 170993, 601361, 122560, 602778, 308230, 602903, 309550, 601788, 602946, 159970, 124092, 180200, 173410, 602356, 603015, 600779, 603111, 187930, 602614, 600951, 603200, 602369, 164770, 147569, 603300, 603301, 159980, 134638,

603431, 147730, 603366, 603348, 600556, 602136, 164160, 310200, 152390,
601241, 116897, 137295, 600576, 194070, 601487, 600698, 164810, 601769, 141900, 602225, 275350, 131100,
179755, 600075, 162200, 165160, 116806, 600899, 123810, 133450, 216400, 278700, 190080, 164730, 191170,
193300, 600618, 600999, 601090, 106150, 601843, 133530, 110700, 602550, 138040, 133430, 300133, 163731,
602302, 126337, 309548, 180245, 126110, 602291, 109565, 107400, 314670, 601444, 143100, 104760, 106180,
601953, 600584, 125852, 602419, 600401, 142200, 107680, 167414, 600020, 188400, 208900, 175100, 602700,
601828, 139320, 602777, 600185, 602681, 603023, 314997, 602848, 600284, 102578, 114290, 165095, 137070,
602991, 602421, 600005, 602996, 314995, 152200, 151900, 112260, 129010, 600892, 273800, 176760, 602341,
490000, 136533, 400003, 601007, 602229, 603620, 602218, 602116, 602020,
142000, 601955, 126340, 120150, 193067, 182452, 142461, 194558, 180660, 600756, 160745, 107741, 106210,
157640, 186770, 146738, 603759, 213700, 147880, 152391, 277900, 151626, 107730, 600711, 600246, 107470,
600237, 223100, 107748, 600065, 600349, 426000, 194500, 154030, 227650, 600247, 314980, 109560, 305370,
600800, 301000, 277700, 600838, 312173, 600439, 600440, 191315, 601595, 190450, 190070, 190020, 162360,
131320, 133540, 600993, 601993, 159530, 601902, 602868, 181590, 601724, 602260, 601093, 187270, 164761,
602102, 603245, 136950, 106100, 601182, 167410, 601897, 602896, 170100, 602506, 104150, 176730, 601600,
187011, 102600, 180380, 162080, 603450, 142967, 602301, 126375, 603372, 603355, 164720, 603250, 167409,
167415, 602897, 601565, 185250, 182138, 601851, 600749, 601575, 194548,
154500, 601365, 194541, 601621, 601623, 601531, 600790, 194355, 123830, 123812, 154540, 601415, 143055,
601386, 194550, 186930, 131290, 601320, 601620, 601754, 601313, 184430, 182900, 182500, 600725, 147870,
154365, 116953, 601297, 601296, 601265, 600796, 120436, 601644, 601930, 601643, 230200, 601645, 601972,
600861, 602009, 601172, 601158, 601646, 180630, 600821, 118440, 601656, 601647, 150200, 601125, 601671,
141850, 116899, 600697, 109270, 202110, 150570, 601108, 191339, 601063, 109691, 180240, 203100, 151430,
179710, 111000, 176797, 238600, 104311, 240300, 125255, 600423, 158070, 602439, 600324, 112261, 243305,
602474, 174762, 600613, 602539, 138890, 138720, 114550, 173865, 602582, 602584, 173510, 600250, 602627,
173325, 602635, 246530, 172425, 600193, 602691, 600188, 170998, 152790,
168468, 256540, 225250, 600848, 143400, 168461, 262600, 168360, 601912, 602951, 600017, 230000, 266600,
602981, 272800, 109150, 102200, 603025, 603026, 603109, 167050, 603127, 603128, 165240, 230400, 313700,
164975, 164875, 602017, 115500, 235800, 164873, 602110, 164785, 164772, 312865, 603296, 600542, 164740,
602125, 309801, 602148, 300007, 306955, 603368, 116940, 602181, 603416, 126650, 163920, 300024, 603437,
602209, 603576, 603607, 305435, 600944, 180410, 303630, 159557, 301870, 132810, 100790, 603849, 603862,
603881,

[0074] There are several methods for analyzing the expression levels of genes associated with diseases. Differences in gene expression levels between diseased and normal tissues are studied by the analytical methods, for example, Northern hybridization and differential display. Other examples include a method with high-density cDNA filter, a method with DNA microarray and methods with PCR amplification (Experimental Medicine, Vol.17, No. 8, 980-1056 (1999); Cell Engineering (additional volume) DNA Microarray and Advanced PCR Methods, Muramatsu & Naba (eds.), Shujunsya). The levels of gene expression between diseased tissues and normal tissues can be studied by any of these analytical methods. When explicit difference in expression level is observed for a gene, it can be concluded that the gene is closely associated with a disease or disorder. Instead of diseased tissues, cultured cells can be used for the assessment. Similarly, when gene expression is explicitly different between normal cells and cells reproducing disease-associated specific features, it can be concluded that the gene is closely associated with a disease or disorder. When the expression levels of genes are evidently varied during major cellular events (such as differentiation and apoptosis), the genes are involved in the cellular events and accordingly are candidates for disease- and/or disorder-associated genes. Further, genes exhibiting tissue-specific expression are genes playing important parts in the tissue functions and, therefore, can be candidates for genes associated with diseases and/or disorders affecting the tissues.

[0075] For example, non-enzymic protein glycation reaction is believed to be a cause for a variety of chronic diabetic complications. Accordingly, in endothelial cells, genes, of which expression levels are elevated or decreased in a glycated protein-dependent manner, are associated with diabetic complications caused by glycated proteins (Diabetes 1996, 45 (Suppl. 3), S67-S72; Diabetes 1997, 46 (Suppl. 2), S19-S25). The onset of rheumatoid arthritis is thought to be involved in the proliferation of synovial cells covering inner surfaces of joint cavity and in inflammatory reaction resulted from the action of cytokines produced by leukocytes infiltrating into the joint synovial tissues (Rheumatism Information Center, http://www.rheuma-net.or.jp/). Recent studies have also revealed that tissue necrosis factor (TNF)-α participates in the onset (Current opinion in immunology 1959, 11, 657-662). When the expression of a gene exhibits responsiveness to the action of TNF on synovial cells, the gene is considered to be involved in rheumatoid arthritis. Many genes acting at the downstream of TNF-. and IL-1. among inflammation-associated cytokines have been previously identified. The respective stimulations are transduced through independent pathways of signaling cascade. There exists another signaling cascade for both stimulations, wherein NF-.B is a common transducing molecule shared by

the two stimulations (J. Leukoc. Biol., 1994, 56(5): 542-547). It has also been revealed that many inflammation-associated genes, including IL-2, IL-6 and G-CSF, are varied in the expression levels in response to the signal through the common pathway (Trends Genet. 1999, 15(6): 229-235). It is assumed that genes of which expression levels are varied in response to the stimulation of TNF-. or IL-1. also participate in inflammation. Genes associated with neural differentiation can be candidates for causative genes for neurological diseases as well as candidates for genes usable for treating the diseases.

[0076] Clones exhibiting differences in the expression levels thereof can be selected by using gene expression analysis. The selection comprises, for example; analyzing cDNA clones by using high-density cDNA filter; and statistically treating the multiple signal values (signal values of radioisotope in the radiolabeled probes or values obtained by measuring fluorescence intensities emitted from the fluorescent labels) for the respective clones by two-sample t-test, where the signal values are determined by multiple experiments of hybridization. The clones of interest are selectable based on the statistically significant differences in the signal distribution at $p<0.05$. However, selectable clones with significant difference in the expression levels thereof may be changed depending on the partial modification of statistical treatment. For example, the clones may be selected by conducting statistical treatment with two-sample t-test at $p<0.01$; or genes exhibiting more explicit differences in the expression levels thereof can be selected by performing statistical treatment with a pre-determined cut-off value for the significant signal difference. An alternative method is that the expression levels are simply compared with each other, and then, the clones of interest are selected based on the ratio of the expression levels thereof.

[0077] Clones exhibiting differences in the expression levels can also be selected by comparing the expression levels by PCR analysis, for example, by using the method of determining the band intensities representing the amounts of PCR products with ethidium bromide staining; the method of determining the radioisotopic signal values or fluorescence intensities of the PCR products when radio-labeled or fluorescence-labeled primers; or the method of determining the values of radioisotope signals or fluorescence intensities of the probes hybridized to the PCR products when radio-labeled or fluorescence-labeled probes, respectively, are used in the hybridization. If the expression level ratios obtained in multiple PCR experiments are constantly at least 2-fold, such a clone can be judged to exhibit the difference in the expression level. When the ratios are several-fold or not less than 10-fold, the clone can be selected as a gene exhibiting the explicit difference in the expression level.

[0078] A survey of genes of which expression levels are varied specifically to the glycated protein in the endothelial cells revealed three genes with elevated expression levels, NT2RP2001538, NT2RP4001001 and Y79AA1000967. These clones are genes associated with diabetes.

[0079] A survey of genes of which expression levels are varied in response to TNF. (Tumor Necrosis Factor-alpha) in the primary cell culture of synovial tissue detected the following clones with elevated expression levels in the presence of TNF.:

BNGH41000020, HEMBA1000349, HEMBA1000634, HEMBA1000671, HEMBA1000835, HEMBA1000962, HEMBA1002178, HEMBA1002195, HEMBA1002239, HEMBA1002420, HEMBA1002524, HEMBA1002992, HEMBA1003315, HEMBA1003392, HEMBA1003487, HEMBA1003602, HEMBA1004067, HEMBA1004797, HEMBA1005337, HEMBA1005489, HEM3A1006916, HEMBB1000668, HEMBB1000905, HEMBB1001547, HEMBB1001573, HEMBB1002041, HEMBB1002663, MAMMA1000652, MAMMA1000810, MAMMA1001634, MAMMA1002091, MAMMA1002234, NT2RM2000306, NT2RM4000417, NT2RP1000002, NT2RP1000181, NT2RP1000740, NT2RP2000694, NT2RP2001921, NT2RP2002527, NT2RP2004495, NT2RP2004606, NT2RP2005163, NT2RP2005463, NT2RP2006134, NT2RP3000171, NT2RP3000652, NT2RP3001195, NT2RP3001976, NT2RP3003473, NT2RP3003874, NT2RP3004090, NT2RP3004294, NT2RP3004557, NT2RP3004647, NT2RP4000108, NT2RP4001001, NT2RP4001877, OVARC1000090, OVARC1000105, OVARC1000275, OVARC1000439, OVARC1001607, PLACE1000740, PLACE1000927, PLACE1001016, PLACE1001100, PLACE1001464, PLACE1001500, PLACE1001918, PLACE1002095, PLACE1002547, PLACE1003644, PLACE1004519, PLACE1005031, PLACE1005410, PLACE1005736, PLACE1006219, PLACE1006809, PLACE1008716, PLACE1010081, THYRO1001770, Y79AA1000127, Y79M1000207, Y79AA1000270, Y79AA1000876, Y794A1001013, Y79AA1001264, Y79AA1001272, Y79AA1001328, Y79AA1001430, Y79AA1001530, Y79AA1001799

[0080] Clones with decreased expression levels in the presence of TNF□ are NT2RM4000326, NT2RP1000300, NT2RP2000514, NT2RP2001755, NT2RP2006042, NT2RP3000481, NT2RP3002790. These clones are candidates for rheumatoid arthritis-associated genes.

[0081] A survey of genes of which expression levels are varied in response to TNF. (Tumor Necrosis Factor-alpha) or IL-1. (Interleukin-1 beta) in a human T cell strain, Jurkat cell, revealed the following clones with elevated expression levels in the presence of TNF.:

MAMMA1000141, MAMMA1000788, MAMMA1001237, MAMMA1002070,NT2RM2000582, NT2RM2002109, NT2RP1000679, NT2RP2003664, NT2RP2004108, NT2RP2005597, NT2RP3001592, NT2RP3002738, NT2RP3004133, NT2RP3004294, NT2RP3004321, NT2RP3004557, PLACE1002547, PLACE1003573,

PLACE1004305, PLACE1008744, PLACE1010011, PLACE1010713, PLACE1011181, Y79AA1000776, Y79AA1002129

[0082] The survey also revealed a clone of which expression level was decreased in the presence of TNF. The clone is PLACE1002070. The same survey further revealed the clones of which expression levels were elevated in the presence of IL-1.. The clones are MAMMA1000614, MAMMA1001237, NT2RM2000514 and NT2RP3001159. These clones are genes associated with inflammation.

[0083] A survey of genes of which expression levels are varied in response to the stimulation for inducing cell differentiation (stimulation using retinoic acid (RA) or using RA/inhibitor (inhibitor for cell division)) in cultured cells of neural strain, NT2, revealed the following clones with elevated expression levels in the presence of RA:

HEMBA1000121, HEMBA1000275, HEMBA1000300, HEMBA1000634, HEMBA1000671, HEMBA1000875, HEMBA1001184, HEMBA1001390, HEMBA1001886, HEMBA1002163, HEMBA1002227, HEMBA1002420, HEMBA1002421, HEMBA1003072, HEMBA1003120, HEMBA1003294, HEMBA1003497, HEMBA1004007, HEMBA1004110, HEMBA1004391, HEMBA1004444, HEMBA1005230, HEMBA1005246, HEMBA1005267, HEMBA1005489, HEMBA1005913, HEMBA1006299, HEMBA1006357, HEMBA1006517, HEMBA1006544, HEMBA1006658, HEMBA1006749, HEMBA1007063, HEMBA1007241, HEMBB1000447, HEMBB1000542, HEMBB1000567, HEMBB1000642, HEMBB1000668, HEMBB1001026, HEMBB1001847, HEMBB1002051, HEMBB1002120, HEMBB1002228, HEMBB1002693, MAMMA1000106, MAMMA1000141, MAMMA1000473, MAMMA1000528, MAMMA1000810, MAMMA1000881, MAMMA1001634, MAMMA1001957, MAMMA1002205, MAMMA1002224, NT2RM2000423, NT2RM2000497, NT2RM2000582, NT2RM2001126, NT2RM2001902, NT2RM4000198, NT2RM4000284, NT2RM4000593, NT2RM4001321, NT2RP1000002, NT2RP1000050, NT2RP1000181, NT2RP1000261, NT2RP1000465, NT2RP1000468, NT2RP1000579, NT2RP1000679, NT2RP2000092, NT2RP2000479, NT2RP2000610, NT2RP2000663, NT2RP2000694, NT2RP2000903, NT2RP2001388, NT2RP2001538, NT2RP2001878, NT2RP2002015, NT2RP2002304, NT2RP2002721, NT2RP2002824, NT2RP2002942, NT2RP2002974, NT2RP2002976, NT2RP2003179, NT2RP2003302, NT2RP2003383, NT2RP2003469, NT2RP2003664, NT2RP2003940, NT2RP2004069, NT2RP2004108, NT2RP2004524, NT2RP2004556, NT2RP2004670, NT2RP2005069, NT2RP2005247, NT2RP2005425, NT2RP2005463, NT2RP2005514, NT2RP2005535, NT2RP2005541, NT2RP2005774, NT2RP2005878, NT2RP2005883, NT2RP2005887, NT2RP2006099, NT2RP2006134, NT2RP3000011, NT2RP3000125, NT2RP3000171, NT2RP3000232, NT2RP3000460, NT2RP3000481, NT2RP3000652, NT2RP3000677, NT2RP3000818, NT2RP3000820, NT2RP3001044, NT2RP3001061, NT2RP3001170, NT2RP3001240, NT2RP3001322, NT2RP3001388, NT2RP3001542, NT2RP3001592, NT2RP3001976, NT2RP3002790, NT2RP3002900, NT2RP3002983, NT2RP3003000, NT2RP3003354, NT2RP3003532, NT2RP3003729, NT2RP3003874, NT2RP3003939, NT2RP3004025, NT2RP3004083, NT2RP3004090, NT2RP3004130, NT2RP3004202, NT2RP3004294, NT2RP3004640, NT2RP4000108, NT2RP4000634, NT2RP4002451, NT2RP4002715, OVARC1000090, OVARC1000208, OVARC1000275, OVARC1000553, OVARC1000775, OVARC1000853, OVARC1000873, OVARC1000916, OVARC1000995, OVARC1001030, OVARC1001049, OVARC1001132, OVARC1001596, OVARC1002178, PLACE1000258, PLACE1000442, PLACE1000927, PLACE1000986, PLACE1001100, PLACE1001123, PLACE1001795, PLACE1002518, PLACE1002547, PLACE1002967, PLACE1003407, PLACE1003428, PLACE1003644, PLACE1003839, PLACE1004078, PLACE1004441, PLACE1004450, PLACE1005669, PLACE1005682, PLACE1005736, PLACE1005768, PLACE1005815, PLACE1006073, PLACE1006208, PLACE1007296, PLACE1007626, PLACE1008282, PLACE1008984, PLACE1008985, PLACE1010445, PLACE1011708, PLACE1011978, PLACE4000455, SKNMC1000004, THYRO1000036, THYRO1000580, THYRO1000776, THYRO1000999, THYRO1001063, THYRO1001128, THYRO1001205, THYRO1001327, THYRO1001523, THYRO1001725, THYRO1001770, Y79AA1000207, Y79AA1000226, Y79AA1000270, Y79AA1001056, Y79AA1001062, Y79AA1001090, Y79AA1001727, Y79AA1002213, Y79AA1002381

[0084] The survey also revealed the clones of which expression levels were decreased in the presence of RA. The clones are BNGH41000020, HEMBA1005070, NT2RP2005027, NT2RP3003473 and Y79AA1002376.

[0085] The same survey further revealed the following clones with elevated expression levels in the presence of RA/inhibitor:

HEMBA1000128, HEMBA1000875, HEMBA1001390, HEMBA1002163, HEMBA1002227, HEMBA1002421, HEMBA1004391, HEMBA1004454, HEMBA1004785, HEMBA1005913, HEMBA1006171, HEMBA1006299, HEMBA1006335, HEMBA1006544, HEMBA1007241, HEMBB1000447, HEMBB1000668, MAMMA1000994, MAMMA1001344, NT2RM2000582, NT2RP1001004, NT2RP2000663, NT2RP2000694, NT2RP2000903, NT2RP2001388, NT2RP2002674, NT2RP2002974, NT2RP2003383, NT2RP2004069, NT2RP2004606, NT2RP2004837, NT2RP2005069, NT2RP2005425, NT2RP2005463, NT2RP2005541, NT2RP2005883, NT2RP2005887, NT2RP3000460, NT2RP3000838, NT2RP3001044, NT2RP3001240, NT2RP3001388,

NT2RP3002721, NT2RP3002738, NT2RP3003469, NT2RP3004083, NT2RP3004130, NT2RP3004202, NT2RP3004294, NT2RP3004640, NT2RP4000108, NT2RP4002451, NT2RP4002715, OVARC1000275, OVARC1000467, OVARC1000553, OVARC1000853, OVARC1000873, OVARC1000916, OVARC1000995, OVARC1001030, OVARC1001222, OVARC1001596, OVARC1002058, OVARC1002178, PLACE1000927, PLACE1001123, PLACE1001407, PLACE1001464, PLACE1001564, PLACE1001795, PLACE1002547, PLACE1003407, PLACE1003644, PLACE1003845, PLACE1004441, PLACE1004482, PLACE1005410, PLACE1005601, PLACE1005725, PLACE1005736, PLACE1006093, PLACE1006219, PLACE1006290, PLACE1006716, PLACE1007296, PLACE1007626, PLACE1008359, PLACE1010968, PLACE1011364, PLACE1011824, THYRO1000678, THYRO1000776, THYRO1000999, THYRO1001113, THYRO1001237, THYRO1001523, Y79AA1000226, Y79AA1000888, Y79AA1001430

[0086] The same survey further revealed the following clones with elevated expression levels in the presence of RA/inhibitor:

HEMBA1000349, HEMBA1001297, HEMBA1001878, HEMBA1005070, HEMBA1006482, HEMBB1001959, NT2RM2001939, NT2RP1000981, NT2RP2001469, NT2RP3003473, OVARC1001132, PLACE1001655, Y79AA1000127, Y79AA1002381. These clones are associated with neural differentiation and, therefore, are candidates for genes associated with neurological diseases.

[0087] Based on the functional analyses using a secretory protein, membrane protein, or proteins associated with signal transduction, glycoprotein, transcription, or diseases, it is possible to develop a medicine.

[0088] In case of a membrane protein, it is most likely to be a protein that functions as a receptor or ligand on the cell surface. Therefore, it is possible to reveal a new relationship between a ligand and receptor by screening the membrane protein of the invention based on the binding activity with the known ligand or receptor. Screening can be performed according to the known methods.

[0089] For example, a ligand against the protein of the invention can be screened in the following manner. Namely, a ligand that binds to a specific protein can be screened by a method comprising the steps of: (a) contacting a test sample with the protein of the invention or a partial peptide thereof, or cells expressing these, and (b) selecting a test sample that binds to said protein, said partial peptide, or said cells.

[0090] On the other hand, for example, screening using cells expressing the protein of the present invention that is a receptor protein can also be performed as follows. It is possible to screen receptors that is capable of binding to a specific protein by using procedures (a) attaching the sample cells to the protein of the invention or its partial peptide, and (b) selecting cells that can bind to the said protein or its partial peptide.

[0091] In a following screening as an example, first the protein of the invention is expressed, and the recombinant protein is purified. Next, the purified protein is labeled, binding assay is performed using a various cell lines or primary cultured cells, and cells that are expressing a receptor are selected (Growth and differentiation factors and their receptors, Shin-Seikagaku Jikken Kouza Vol.7 (1991) Honjyo, Arai, Taniguchi, and Muramatsu edit, p203-236, Tokyo-Kagaku-Doujin). A protein of the invention can be labeled with RI such as ^{125}I, and enzyme (alkaline phosphatase etc.). Alternatively, a protein of the invention may be used without labeling and then detected by using a labeled antibody against the protein. The cells that are selected by the above screening methods, which express a receptor of the protein of the invention, can be used for the further screening of an agonists or antagonists of the said receptor.

[0092] Once the ligand binding to the protein of the invention, the receptor of the protein of the invention or the cells expressing the receptor are obtained by screening, it is possible to screen a compound that binds to the ligand and receptor. Also it is possible to screen a compound that can inhibit both bindings (agonists or antagonists of the receptor, for example) by utilizing the binding activities.

[0093] When the protein of the invention is a receptor, the screening method comprises the steps of (a) contacting the protein of the invention or cells expressing the protein of the invention with the ligand, in the presence of a test sample, (b) detecting the binding activity between said protein or cells expressing said protein and the ligand, and (c) selecting a compound that reduces said binding activity when compared to the activity in the absence of the test sample. Furthermore, when the protein of the invention is a ligand, the screening method comprises the steps of (a) contacting the protein of the invention with its receptor or cells expressing the receptor in the presence of samples, (b) detecting the binding activity between the protein and its receptor or the cells expressing the receptor, and (c) selecting a compound that can potentially reduce the binding activity compared to the activity in the absence of the sample.

[0094] Samples to screen include cell extracts, expressed products from a gene library, synthesized low molecular compound, synthesized peptide, and natural compounds, for example, but are not construed to be listed here. A compound that is isolated by the above screening using a binding activity of the protein of the invention can also be used as a sample.

[0095] A compound isolated by the screening may be a candidate to be an agonist or an antagonist of the receptor of the protein. By utilizing an assay that monitors a change in the intracellular signaling such as phosphorylation which results from reduction of the binding between the protein and its receptor, it is possible to identify whether the obtained compound is an agonist or antagonist of the receptor. Also, the compound may be a candidate of a molecule that can

inhibit the interaction between the protein and its associated proteins (including a receptor) in vivo. Such compounds can be used for developing drugs for precaution or cures of a disease with which the protein is associated.

[0096] Secretory proteins may regulate cellular conditions such as growth and differentiation. It is possible to find out a novel factor that regulates cellular conditions by adding the secretory protein of the invention to a certain kind of cell, and performing a screening by utilizing the cellular changes in growth or differentiation, or activation of a particular gene.

[0097] The screening can be performed, for example, as follows. First, the protein of the invention is expressed and purified in a recombinant form. Then, the purified protein is microinjectedadded into a various kind of cell lines or primary cultured cells, and the change in the cell growth and differentiation is monitored. The induction of a particular gene that is known to be involved in a certain cellular change is detected with the amounts of mRNA and protein. Alternatively, the amount of an intracellular molecule (low molecular compounds, etc.) that is changed by the function of a gene product (protein) that is known to be functioning in a certain cellular change is used for the detection.

[0098] Once the screening reveals that the protein of the invention can regulate cellular conditions or the functions, it is possible to apply the protein as a pharmaceutical and diagnostic medicine for associated diseases by itself or by altering a part of it into an appropriate composition.

[0099] As is above described for membrane proteins, the secretory protein provided by the invention may be used to explore a novel ligand-receptor interaction using a screening based on the binding activity to a known ligand or receptor. A similar method can be used to identify an agonist or antagonist. The resulting compounds obtained by the methods can be a candidate of a compound that can inhibit the interaction between the protein of the invention and an interacting molecule (including a receptor). The compounds may be able to use as a preventive, therapeutic, and diagnostic medicine for the diseases, in which the protein may play a certain role.

[0100] Proteins associated with signal transduction or transcription may be a factor that affects a certain protein or gene in response to intracellular/extracellular stimuli. It is possible to find out a novel factor that can affect a protein or gene by expressing the protein provided by the invention in a certain types of cells, and performing a screening utilizing the activation of a certain intracellular protein or gene.

[0101] The screening may be performed as follows. First, a transformed cell expressing the protein is obtained. Then, the transformed cell line and the untransformed original cell are compared for the changes in the expression of a certain gene by detecting the amount of its mRNA or protein. Alternatively, the amount of an intracellular molecule (low molecular compounds), which is changed by the function of a gene product (protein) that is known to function in a certain cellular change, may be used for the detection. Furthermore, the change of the expression of a certain gene can be detected by introducing a fusion gene that comprises a regulatory region of the gene and a marker gene (luciferase, beta-galactosidase, etc.) into a cell, expressing the protein provided by the invention into the cell, and estimating the activity of a marker gene product (protein).

[0102] If the protein or gene of the invention is associated with diseases, it is possible to screen a gene or compound that can regulate its expression and/or activity either directly or indirectly by utilizing the protein of the present invention.

[0103] For example, the protein of the invention is expressed and the recombinant protein is purified. Then, the protein and gene whose expression was affected in the presence of the protein of the invention is also purified, and the binding activity between the two proteins or genes is examined. The examination may be performed with pretreatment with a compound that is candidate of an inhibitor. In an alternative method, a transcription regulatory region locating in the 5'-upstream of the gene encoding the protein of the invention that is capable of regulating the expression of other genes is obtained, and fused with a marker gene. The fusion is introduced into a cell, and the cell is added with compounds to explore a regulatory factor of the expression of the said gene.

[0104] The compound obtained by the screening can be used for developing pharmaceutical and diagnostic medicines for the diseases with which the protein of the present invention is associated. Similarly, if the regulatory factor obtained by the screening is a protein, the protein itself can be used as a pharmaceutical, and if there is a compound that affects the original expression level and/or activity of the protein, it also can be used for the same purpose.

[0105] If the protein of the invention has an enzymatic activity, regardless of whether it is a secretory protein, membrane protein, or proteins associated with signal transduction, glycoprotein, transcription, or diseases, a screening may be performed by adding a compound to the protein of the invention under the suitable condition and monitoring the change of the compound. The enzymatic activity may also be utilized to screen for a compound that can inhibit the activity of the protein.

[0106] In a screening given as an example, the protein of the invention is expressed and the recombinant protein is purified. Then, compounds are contacted with the purified protein, and the amount of the compound and the reaction products is examined. Alternatively, compounds that are candidates of an inhibitor are pretreated, then a compound (substrate) that can react with the purified protein is added, and the amount of the substrate and the reaction products is examined.

[0107] The compounds obtained in the screening may be used as a medicine for diseases with which the protein of the invention is associated. Also they can be applied for tests that examine whether the protein of the invention functions

normally *in vivo.*

[0108] Whether the secretory or membrane protein of the present invention is a novel protein associated with diseases or not is determined in another method than described above, by obtaining a specific antibody against the protein of the invention, and examining the relationship between the expression or activity of the protein and a certain disease. In an alternative way, it may be analyzed referred to the methods in "Molecular Diagnosis of Genetic Diseases" (Elles R. edit, (1996) in the series of "Method in Molecular Biology" (Humana Press).

[0109] Disease-associated proteins are a target of the above described screenings and very useful for developing a drug that is capable of regulating the expression and activity of the protein. Also, they are useful in medicinal industry as a diagnostic marker of the related disease and as a target for gene therapy.

[0110] Compounds isolated as mentioned above can be administered patients as it is, or after formulated into a pharmaceutical composition according to the known methods. For example, a pharmaceutically acceptable carrier or vehicle, specifically sterilized water, saline, plant oil, emulsifier, or suspending agent can be mixed with the compounds appropriately. The pharmaceutical compositions can be administered to patients by a method known to those skilled in the art, such as intraarterial intravenous, or subcutaneous injections. The dosage may vary depending on the weight or age of a patient, or the method of administration, but those skilled in the art can choose an appropriate dosage properly. If the compound is encoded by DNA, the DNA can be cloned into a vector for gene therapy, and used for gene therapy. The dosage of the DNA and the method of its administration may vary depending on the weight or age of a patient, or the symptoms, but those skilled in the art can choose properly.

[0111] The protein encoded by the polynucleotide of the invention can be prepared as a recombinant protein or as a natural protein. For example, the recombinant protein can be prepared by inserting the polynucleotide encoding the protein of the invention into a vector, introducing the vector into an appropriate host cell and purifying the protein expressed within the transformed host cell, as described below. In contrast, the natural protein can be prepared, for example, by utilizing an affinity column to which an antibody against the protein of the invention (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 16.1-16.19) is attached. The antibody used for the affinity purification may be either a polyclonal antibody, or a monoclonal antibody. Alternatively, in vitro translation (See, for example, "On the fidelity of mRNA translation in the nuclease-treated rabbit reticulocyte lysate system." Dasso M.C., and Jackson R.J. (1989) Nucleic Acids Res. 17: 3129-3144) may be used for preparing the protein of the invention.

[0112] Proteins functionally equivalent to the proteins of the present invention can be prepared based on the activities, which were clarified in the above-mentioned manner, of the proteins of the present invention. Using the biological activity possessed by the protein of the invention as an index, it is possible to verify whether or not a particular protein is functionally equivalent to the protein of the invention by examining whether or not the protein has said activity.

[0113] Proteins functionally equivalent to the proteins of the present invention can be prepared by those skilled in the art, for example, by using a method for introducing mutations into an amino acid sequence of a protein (for example, site-directed mutagenesis (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 8.1-8.5). Besides, such proteins can be generated by spontaneous mutations. The present invention comprises the proteins having one or more amino acid substitutions, deletions, insertions and/or additions in the amino acid sequences of the proteins of the present invention (Table 370), as far as the proteins have the equivalent functions to those of the proteins identified in the present Examples described later.

[0114] There are no limitations in the number and sites of amino acid mutations, as far as the proteins maintain the functions thereof. The number of mutations is typically 30% or less, or 20% or less, or 10% or less, preferably within 5% or less, or 3% or less of the total amino acids, more preferably within 2% or less or 1% or less of the total amino acids. From the viewpoint of maintaining the protein function, it is preferable that a substituted amino has a similar property to that of the original amino acid. For example, Ala, Val, Leu, Ile, Pro, Met, Phe and Trp are assumed to have similar properties to one another because they are all classified into a group of non-polar amino acids. Similarly, substitution can be performed among non-charged amino acid such as Gly, Ser, Thr, Cys, Tyr, Asn, and Gln, acidic amino acids such as Asp and Glu, and basic amino acids such as Lys, Arg, and His.

[0115] In addition, proteins functionally equivalent to the proteins of the present invention can be isolated by using techniques of hybridization or gene amplification known to those skilled in the art. Specifically, using the hybridization technique (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4)), those skilled in the art can usually isolate a DNA highly homologous to the DNA encoding the protein identified in the present Example based on the identified nucleotide sequence (Table 370) or a portion thereof and obtain the functionally equivalent protein from the isolated DNA. The present invention includes proteins encoded by the DNAs hybridizing with the DNAs encoding the proteins identified in the present Example, as far as the proteins are functionally equivalent to the proteins identified in the present Example. Organisms from which the functionally equivalent proteins are isolated are illustrated by vertebrates such as human, mouse, rat, rabbit, pig and bovine, but are not limited to these animals.

[0116] Washing conditions of hybridization for the isolation of DNAs encoding the functionally equivalent proteins are usually "1xSSC, 0.1% SDS, 37"; more stringent conditions are "0.5xSSC, 0.1% SDS, 42."; and still more stringent conditions are "0.1 x SSC, 0.1% SDS, 65.". Alternatively, the following conditions can be given as hybridization con-

ditions of the present invention. Namely, conditions in which the hybridization is done at "6xSSC, 40% Formamide, 25.", and the washing at "1xSSC, 55." can be given. More preferable conditions are those in which the hybridization is done at "6xSSC, 40% Formamide, 37.", and the washing at "0.2xSSC, 55,". Even more preferable are those in which the hybridization is done at "6xSSC, 50% Formamide, 37.", and the washing at "0.1xSSC, 62.". The more stringent the conditions of hybridization are, the more frequently the DNAs highly homologous to the probe sequence are isolated. Therefore, it is preferable to conduct hybridization under stringent conditions. Examples of stringent conditions in the present invention are, washing conditions of "0.5xSSC, 0.1% SDS, 42.", or alternatively, hybridization conditions of "6xSSC, 40% Formamide, 37.", and the washing at "0.2xSSC, 55.". However, the above-mentioned combinations of SSC, SDS and temperature conditions are indicated just as examples. Those skilled in the art can select the hybridization conditions with similar stringency to those mentioned above by properly combining the above-mentioned or other factors (for example, probe concentration, probe length and duration of hybridization reaction) that determines the stringency of hybridization.

[0117] The amino acid sequences of proteins isolated by using the hybridization techniques usually exhibit high homology to those of the proteins of the present invention, which are shown in Table 370. The present invention encompasses a polynucleotide comprising a nucleotide sequence that has a high identity to the nucleotide sequence of claim 8 (a). Furthermore, the present invention encompasses a peptide, or protein comprising an amino acid sequence that has a high identity to the amino acid sequence encoded by the polynucleotide of claim 8 (b). The term "high identity" indicates sequence identity of at least 40% or more; preferably 60% or more; and more preferably 70% or more. Alternatively, more preferable is identity of 90% or more, or 93% or more, or 95% or more, furthermore, 97% or more, or 99% or more. The identity can be determined by using the BLAST search algorithm.

[0118] With the gene amplification technique (PCR) (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4)) using primers designed based on the nucleotide sequence (Table 370) or a portion thereof identified in the present Example, it is possible to isolate a DNA fragment highly homologous to the nucleotide sequence or a portion thereof and to obtain functionally equivalent protein to a particular protein identified in the present Example based on the isolated DNA fragment.

[0119] The "percent identity" of two amino acid sequences or of two nucleic acids is determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sei. USA 87:2264-2268, 1990), modified as in Karlin and Altschul (Proc. Natl. Acad. Sei. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul et al. (J. Mol. Biol.215:403-410, 1990). BLAST nucleotide searches are performed with the BLASTN program, score = 100, wordlength = 12. BLAST protein searches are performed with the BLASTX program, score = 50, wordlength = 3. When gaps exist between two sequences, Gapped BLAST is utilized as described in Altschul et al. (Nucleic Acids Res.25:3389-3402,1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., BLASTX and BLASTN) are used. See http://www.ncbi.nlm.nih.gov.

[0120] The present invention also includes a partial peptide of the proteins of the invention. The partial peptide comprises a protein generated as a result that a signal peptide has been removed from a secretory protein. If the protein of the present invention has an activity as a receptor or a ligand, the partial peptide may function as a competitive inhibitor of the protein and may bind to the receptor (or ligand). In addition, the present invention comprises an antigen peptide for raising antibodies. For the peptides to be specific for the protein of the invention, the peptides comprise at least 7 amino acids, preferably 8 amino acids or more, more preferably 9 amino acids or more, and even more preferably 10 amino acids or more. The peptide can be used for preparing antibodies against the protein of the invention, or competitive inhibitors of them, and also screening for a receptor that binds to the protein of the invention. The partial peptides of the invention can be produced, for example, by genetic engineering methods, known methods for synthesizing peptides, or digesting the protein of the invention with an appropriate peptidase.

[0121] The present invention also relates to a vector into which the DNA of the invention is inserted. The vector of the invention is not limited as long as it contains the inserted DNA stably. For example, if E. coli is used as a host, vectors such as pBluescript vector (Stratagene) are preferable as a cloning vector. To produce the protein of the invention, expression vectors are especially useful. Any expression vector can be used as far as it is capable of expressing the protein in vitro, in E. coli, in cultured cells, or in vivo. For example, pBEST vector (Promega) is preferable for in vitro expression, pET vector (Invitrogen) for E. coli, pME18S-FL3 vector (GenBank Accession No. AB009864) for cultured cells, and pME18S vector (Mol. Cell. Biol. (1988) 8: 466-472) for in vivo expression. To insert the DNA of the invention, ligation utilizing restriction sites can be performed according to the standard method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 11.4-11.11).

[0122] The present invention also relates to a transformant carrying the vector of the invention. Any cell can be used as a host into which the vector of the invention is inserted, and various kinds of host cells can be used depending on the purposes. For strong expression of the protein in eukaryotic cells, COS cells or CHO cells can be used, for example.

[0123] Introduction of the vector into host cells can be performed, for example, by calcium phosphate precipitation method, electroporation method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 9.1-9.9), lipofectamine method (GIBCO-BRL), or microinjection method, etc.

[0124] The primer of the present invention can be used for synthesizing full-length cDNA, and also for the detection and/or diagnosis of the abnormality of the protein of the invention encoded by the full-length cDNA. For example, by utilizing polymerase chain reaction (genomic DNA-PCR, or RT-PCR) using the primer of the invention, DNA encoding the protein of the invention can be amplified. It is also possible to obtain the regulatory region of expression in the 5'-upstream by using PCR or hybridization since the transcription start site within the genomic sequence can be easily specified based on the 5'-end sequence of the full-length cDNA. The obtained genomic region can be used for detection and/or diagnosis of the abnormality of the sequence by RFLP analysis, SSCP, or direct sequencing.

[0125] Furthermore, the "polynucleotide having a length of at least 15 nucleotides, comprising a nucleotide sequence that is complementary to a polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs in Table 370, or its complementary strand" includes an antisense polynucleotide for suppressing the expression of the protein of the invention. To exert the antisense effect, the antisense polynucleotide has a length of at least 15 bp or more, for example, 50 bp or more, preferably 100 bp or more, and more preferably 500 bp or more, and has a length of usually 3000 bp or less and preferably 2000 bp or less. The antisense DNA can be used in the gene therapy of the diseases that are caused by the abnormality of the protein of the invention (abnormal function or abnormal expression). Said antisense DNA can be prepared, for example, by the phosphorothioate method ("Physicochemical properties of phosphorothioate oligodeoxynucleotides." Stein (1988) Nucleic Acids Res. 16: 3209-3221) based on the nucleotide sequence of the DNA encoding the protein (for example, the DNA set forth in any one of SEQ ID NOs in Table 370).

[0126] The polynucleotide or antisense DNA of the present invention can be used in gene therapy, for example, by administrating it into a patient by the in vivo or ex vivo method with virus vectors such as retrovirus vectors, adenovirus vectors, and adeno-associated virus vectors, or non-virus vectors such as liposome.

[0127] The present invention also relates to antibodies that bind to the protein of the invention. There are no limitations in the form of the antibodies of the invention. They include polyclonal antibodies, monoclonal antibodies, or their portions that can bind to the protein of the invention. They also include antibodies of all classes. Furthermore, special antibodies such as humanized antibodies are also included.

[0128] The polyclonal antibody of the invention can be obtained according to the standard method by synthesizing an oligopeptide corresponding to the amino acid sequence and immunizing rabbits with the peptide (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 11.12-11.13). The monoclonal antibody of the invention can be obtained according to the standard method by purifying the protein expressed in E. coli, immunizing mice with the protein, and producing a hybridoma cell by fusing the spleen cells and myeloma cells (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 11.4-11.11).

[0129] The antibody binding to the protein of the present invention can be used for purification of the protein of the invention, and also for detection and/or diagnosis of the abnormalities of the expression and structure of the protein. Specifically, proteins can be extracted, for example, from tissues, blood, or cells, and the protein of the invention is detected by Western blotting, immunoprecipitation, or ELISA, etc. for the above purpose.

[0130] Furthermore, the antibody binding to the protein of the present invention can be utilized for treating the diseases that associates with the protein of the invention. If the antibodies are used for treating patients, human antibodies or humanized antibodies are preferable in terms of their low antigenicity. The human antibodies can be prepared by immunizing a mouse whose immune system is replaced with that of human ("Functional transplant of megabase human immunoglobulin loci recapitulates human antibody response in mice" Mendez M.J. et al. (1997) Nat. Genet. 15: 146-156). The humanized antibodies can be prepared by recombination of the hypervariable region of a monoclonal antibody (Methods in Enzymology (1991) 203: 99-121).

[0131] The present invention further relates to databases comprising at least a sequence of polynucleotide and/or protein, or a medium recorded in such databases, selected from the sequence data of the nucleotide and/or the amino acids indicated in Table 370. The term "database" means a set of accumulated information as machine-searchable and readable information of nucleotide sequence. The databases of the present invention comprise at least one of the novel nucleotide sequences of polynucleotide provided by the present invention. The databases of the present invention can consist of only the sequence data of the polynucleotide provided by the present invention or can comprise other information on nucleotide sequences of known full-length cDNAs or ESTs. The databases of the present invention can be comprised of not only the information on the nucleotide sequences but also the information on the gene functions revealed by the present invention. Additional information such as names of DNA clones carrying the full-length cDNAs can be recorded or linked together with the sequence data in the databases.

[0132] The database of the present invention is useful for gaining complete gene sequence information from partial sequence information of a gene of interest. The database of the present invention comprises nucleotide sequence information of full-length cDNAs. Consequently, by comparing the information in this database with the nucleotide sequence of a partial gene fragment yielded by differential display method or subtraction method, the information on the full-length nucleotide sequence of interest can be gained from the sequence of the partial fragment as a starting clue.

[0133] The sequence information of the full-length cDNAs constituting the database of the present invention contains not only the information on the complete sequences but also extra information on expression frequency of the genes

as well as homology of the genes to known genes and known proteins. Thus the extra information facilitates rapid functional analyses of partial gene fragments. Further, the information on human genes is accumulated in the database of the present invention, and therefore, the database is useful for isolating a human homologue of a gene originating from other species. The human homologue can be isolated based on the nucleotide sequence of the gene from the original species.

[0134] At present, information on a wide variety of gene fragments can be obtained by differential display method and subtraction method. In general, these gene fragments are utilized as tools for isolating the full-length sequences thereof. When the gene fragment corresponds to an already-known gene, the full-length sequence is easily obtained by comparing the partial sequence with the information in known databases. However, when there exists no information corresponding to the partial sequence of interest in the known databases, cDNA cloning should be carried out for the full-length cDNA. It is often difficult to obtain the full-length nucleotide sequence using the partial sequence information as an initial clue. If the full-length of the gene is not available, the amino acid sequence of the protein encoded by the gene remains unidentified. Thus the database of the present invention can contribute to the identification of full-length cDNAs corresponding to gene fragments, which cannot be revealed by using databases of known genes.

[0135] The invention is illustrated more specifically with reference to the following examples, but is not to be construed as being limited thereto.

EXAMPLE 1

Construction of a cDNA library by the oligo-capping method.

[0136] The NT-2 neuron progenitor cells (Stratagene), a teratocarcinoma cell line from human embryo testis, which can differentiate into neurons by treatment with retinoic acid were used. The NT-2 cells were cultured according to the rnanufacturer's instructions as follows.

(1) NT-2 cells were cultured without induction by retinoic acid treatment ((NT2RM1, NT2RM2, NT2RM4)).
(2) After cultured, NT-2 cells were induced by adding retinoic acid, and then were cultured for 48 hours (NT2RP1).
(3) After cultured, NT-2 cells were induced by adding retinoic acid, and then were cultured for 2 weeks (NT2RP2, NT2RP3, NT2RP4).

[0137] Also, the human brain neuroglioma cell line H4 (ATCC HTG-148) (BNGH41), human neuroblastoma cell line SK-N-MC (ATCC HTB-10) (SKNMC1), and human retinoblastoma cell line Y79 (ATCC HTB-18) (Y79AA1) were cultured according to the culture conditions described in the ATCC catalogue. The cells were harvested separately, and mRNA was extracted from each cell by the method described in the literature (Molecular Cloning 2nd edition. Sambrook J., Fritsch, E.F., and Maniatis T. (1989) Cold Spring Harbor Laboratory Press). Furthermore, poly(A)$^+$RNA was purified from the mRNA using oligo-dT cellulose.

[0138] Similarly, human placenta (PLACE1, PLACE2, PLACE3), human ovary cancer tissue (OVARC1), tissues from human embryo at 10 weeks, which is enriched with head (HEMBA1), or body (HEMBB1), human mammary gland (MAMMA1), human thyroid gland (THYRO1) were used to extract mRNA by the method described in the literature (Molecular Cloning 2nd edition. Sambrook J., Fritsch, E.F., and Maniatis T. (1989) Cold Spring Harbor Laboratory Press). Furthermore, poly(A)$^+$RNA was purified from the mRNA using oligo-dT cellulose.

[0139] Each poly(A)$^+$RNA was used to construct a cDNA library by the oligo-capping method (Maruyama M. and Sugano S. (1994) Gene 138: 171-174). Using the Oligo-cap linker (SEQ ID NO: 2541) and the Oligo-dT primer (SEQ ID NO: 2542), bacterial alkaline phosphatase (BAP) treatment, tobacco acid phosphatase (TAP) treatment, RNA ligation, the first strand cDNA synthesis, and removal of RNA were performed as described in the reference (Suzuki and Kanno (1996) Protein Nucleic acid and Enzyme. 41: 197-201; Suzuki Y. et al. (1997) Gene 200: 149-156). Next, 5'- and 3'-PCR primers (SEQ ID NO: 2543, and 2544, respectively) were used for performing PCR to convert the cDNA into double stranded cDNA, which was then digested with SfiI. Then, the DraIII-cleaved pUC19FL3 vector (Figure 1; for NT2RM1, and NT2RP1), or the DraIII-cleaved pME18SFL3 (Figure 1) (GenBank AB009864; expression vector; for NT2RM2, NT2RM4, NT2RP2, NT2RP3, NT2RP4, BNGH41, SKNMC1, Y79AA1, PLACE1, PLACE2, PLACE3, OVARC1, HEMBA1, HEMBB1, MAMMA1, and THYRO1) was used for cloning the cDNA in an unidirectional manner, and cDNA libraries were obtained. Then, the nucleotide sequence of the 5'- and 3'- ends of the cDNA clones was analyzed with a DNA sequencer (ABI PRISM 377, PE Biosystems) after sequencing reactions were performed with the DNA sequencing reagents (Dye Terminator Cycle Sequencing FS Ready Reaction Kit, dRhodamine Terminator Cycle Sequencing FS Ready Reaction Kit, or BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, from by PE Biosystems) according to the instructions. The data were compiled into a database.

[0140] The full-length-enriched cDNA libraries except those for NT2RM1 and NT2RP1 were constructed using eukaryotic expression vector pME18SFL3. The vector contains SRα promoter and SV40 small t intron in the upstream

of the cloning site, and SV40 polyA added signal sequence site in the downstream. As the cloning site of pME18SFL3 has asymmetrical DraIII sites, and the ends of cDNA fragments contain SfiI sites complementary to the DraIII sites, the cloned cDNA fragments can be inserted into the downstream of the SRα promoter unidirectionally. Therefore, clones containing full-length cDNA can be expressed transiently by introducing the obtained plasmid directly into COS cells. Thus, the clones can be analyzed very easily in terms of the proteins that are the gene products of the clones, or in terms of the biological

[0141] Herein, the cDNA libraries and the name of each clone are related as shown in Table 2. Therein, "xxxxxx" represents the clone number of six digits. Thus, the sequences are named by the library name, the clone number plus F- for the 5'-end, or R- for the 3'-end.

Table 2

library: clone	5'-end sequence	3'-end sequence
NT2RM1:		
NT2RM1xxxxxx	F-NT2RM1xxxxxx	
NT2RP1:		
NT2RP1xxxxxx	F-NT2RP1xxxxxx	
NT2RM2:		
NT2RM2xxxxxx	F-NT2RM2xxxxxx	R-NT2RM2xxxxxx
NT2RM4:		
NT2RM4xxxxxx	F-NT2RM4xxxxxx	R-NT2RM4xxxxxx
NT2RP2:		
NT2RP2xxxxxx	F-NT2RP2xxxxxx	R-NT2RP2xxxxxx
NT2RP3:		
NT2RP3xxxxxx	F-NT2RP3xxxxxx	R-NT2RP3xxxxxx
NT2RP4:		
NT2RP4xxxxxx	F-NT2RP4xxxxxx	R-NT2RP4xxxxxx
BNGH41:		
BNGH41xxxxxx	F-BNGH41xxxxxx	R-BNGH41xxxxxx
SKNMC1:		
SKNMC1xxxxxx	F-SKNMC1xxxxxx	R-SKNMC1xxxxxx
Y79AA1:		
Y79AA1xxxxxx	F-Y79AA1xxxxxx	R-Y79AA1xxxxxx
PLACE1:		
PLACE1xxxxxx	F-PLACE1xxxxxx	R-PLACE1xxxxxx
PLACE2:		
PLACE2xxxxxx	F-PLACE2xxxxxx	R-PLACE2xxxxxx
PLACE3:		
PLACE3xxxxxx	F-PLACE3xxxxxx	R-PLACE3xxxxxx
OVARC1:		
OVARC1xxxxxx	F-OVARC1xxxxxx	R-OVARC1xxxxxx
HEMBA1:		
HEMBA1xxxxxx	F-HEMBA1xxxxxx	R-HEMBA1xxxxxx
HEMBB1:		
HEMBB1xxxxxx	F-HEMBB1xxxxxx	R-HEMBB1xxxxxx
MAMMA1:		
MAMMA1xxxxxx	F-MAMMA1xxxxxx	R-MAMMA1xxxxxx
THYRO1:		

THYRO1xxxxxx F-THYRO1xxxxxx R-THYRO1xxxxxx

EXAMPLE 2

Estimation of the fullness ratio of the 5'-ends of the clones contained in the cDNA libraries constructed by the oligo-capping method.

[0142] The fullness ratio at the 5'-end sequences of the 59,823 clones in the human cDNA libraries constructed by the oligo-capping method was determined as follows. Of all the clones whose 5'-end sequences were found in those of known human mRNA in the public database, a clone was judged to be "full-length", if it had a longer 5'-end sequence than that of the known human mRNA, or, even though the 5'-end sequence was shorter, if it contained the translation initiation codon. A clone which did not contain the translation initiation codon was judged to be "non-full-length". The fullness ratio ((the number of full-length clones)/(the number of full-length and non-full-length clones)) at the 5'-end of the cDNA clones from each library was determined by comparing with the known human mRNA. As a result, the fullness ratio of the 5'-ends was 63.5%. It suggests that the human cDNA clones obtained by the described method have complete 5'-ends with high probability.

EXAMPLE 3

Assessment of the fullness ratio of the 5'-end of the cDNA by the ATGpr and the ESTiMateFL.

[0143] The ATGpr, developed by Salamov A.A., Nishikawa T., and Swindells M.B. in the Helix Research Institute, is a program for prediction of the translation start codon based on the characteristics of the sequences in the vicinity of the ATG codon. The results are shown with expectations that an ATG is a true start codon (0.05-0.94). When this program is applied to general cDNAs without considering whether or not the ATG codons in the cDNAs are the true initiation codons of the cDNAs, both the sensitivity and the specificity of the results are estimated at 66%. Here, the sensitivity means the ratio of the number of codons judged to be initiation codons by the program to the total number of true initiation codons, and the specificity means the ratio of the number of true initiation codons to the number of codons judged to be initiation codons by the program. In contrast, when the program was applied to the 5'-end sequences of the clones from the cDNA library that was obtained by the oligo-capping method and that had 65% fullness ratio, the sensitivity and specificity of evaluation of a full-length clone (clone containing the N-terminal end of ORF) were improved to 82-83% by selecting only clones having the ATGpr1 score 0.6 or higher.

[0144] Furthermore, the program was used to assess the fullness of 18,959 clones in the human cDNA libraries obtained here, which have 5'-ends matched to a known human mRNA. Briefly, the maximal ATGpr1 score of the clones was determined, and then their 5'-end sequence was compared with the known human mRNA to estimate whether the clone is full-length or not. The result was summarized in Table 3. Based on the knowledge that known mRNAs, in general, are highly expressed in the cell, the expression levels of genes having a low number in the EST hit, which represent mRNAs whose expression levels are relatively low were examined, and the result is shown in Table 4.

[0145] In the table, the number of full-length clones indicate that of clones containing the N-terminal end of ORF, and so does the number of non-full-length clones that of clones without the N-terminal end of ORF. The fullness ratio represents (the number of full-length clones)/(the number of full-length clones plus the number of non-full-length clones).

Table 3

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequences of clones obtained from human cDNA libraries constructed by the oligo-capping method; clones having a matched 5'-end with that of a known human mRNA.

maximal ATGpr1 score	number of (full-length clones plus non-full-length clones)	number of full-length clones	fullness ratio
>=0.70	11,193	9,346	83.5%
>=0.50	13,369	10,549	78.9%
>=0.30	15,489	11,340	73.2%

Table 3 (continued)

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequences of clones obtained from human cDNA libraries constructed by the oligo-capping method; clones having a matched 5'-end with that of a known human mRNA.			
maximal ATGpr1 score	number of (full-length clones plus non-full-length clones)	number of full-length clones	fullness ratio
>=0.15	17,394	11,811	67.9%
>=0.00	18,959	12,046	63.5%

Table 4

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequences of the clones obtained from human cDNA libraries constructed by the oligo-capping method; clones having 5 EST hits or less among the clones having a matched 5'-end with that of a known human mRNA.			
maximal ATGpr1 score	number of (full-length clones plus non-full-length clones)	number of full-length clones	fullness ratio
>=0.70	2,801	1,934	69.0%
>=0.50	3,683	2,393	65.0%
>=0.30	4,683	2,707	57.8%
>=0.15	5,559	2,890	52.0%
>=0.00	6,113	3,013	49.8%

[0146] The ESTiMateFL, developed by Nishikawa and Ota in the Helix Research Institute, is a method for the selection of a clone with high fullness ratio by comparing with the 5'-end or 3'-end sequences of ESTs in the public database.

[0147] By the method, a cDNA clone is judged presumably not to be full-length if there exist any ESTs which have longer 5'-end or 3'-end sequences than the clone. The method is systematized for high throughput analysis. A clone is judged to be full-length if the clone has a longer 5'-end sequence than ESTs in the public database. Even if a clone has a shorter 5'-end, the clone is judged to be full-length if the difference in length is within 50 bases, and otherwise judged not to be full-length, for convenience. In case of the 5'-end sequence of the clones which matches a known mRNA, about 80% of the sequences that were judged to be full-length by comparing with ESTs was judged to be full-length by estimating the 5'-end sequence, as well; about 80% of the sequences that were judged to be not full-length by comparing with ESTs was judged to be not full-length by estimating the 5'-end sequence, as well. The accuracy of the prediction by comparing cDNA clones with ESTs is improved with increasing number of ESTs to be compared. However, when only a limited number of ESTs are available, the reliability becomes low. Thus, the method is effective in excluding clones with high probability of being non-full-length, from the cDNA clones that is synthesized by the oligo-capping method and that have the 5'-end sequences with about 60 % fullness ratio. In particular, the ESTiMateFL is efficiently used to estimate the fullness ratio at the 3'-end sequence of cDNA of a human unknown mRNA which has a significant number of ESTs in the public database.

[0148] The 18,959 clones isolated from human cDNA libraries constructed by the oligo-capping method, which have the 5'-end sequence that matches a known human mRNA, were estimated by using the ATGpr and ESTiMateFL. Briefly, the 5'-end sequence that matches a known human mRNA of the respective clone was analyzed to obtain the maximal ATGpr1 score, and compared with the ORF of the known human mRNA that matches it to determine whether the clone is full-length or not. Then, the 5'-end sequence of the respective clone was analyzed by the ESTiMateFL to judge whether the clone is full-length or not. Specifically, the 5'-end sequences that match a known human mRNA of the 18,959 clones constructed by the oligo-capping method were compared with those of ESTs by the ESTiMateFL and the clones other than those that are not full-length were selected. Then, the selected clones were used to analyze the relationship between the ATGpr and the fullness ratio. The result was summarized in Table 5. Also, among the selected, the clones in which the number of the EST hit is not more than 5 were selected and analyzed. The result was summarized in Table 6, which represents the result of the analysis of mRNA with relatively low abundance.

[0149] In the Tables, the number of full-length clones, the number of non-full-length clones, and the fullness ratio indicate the number of the clones that contain the N-terminus of the ORF, the number of the clones that do not contain

the N-terminus of the ORF, and (the number of full-length clones)/(the number of full-length clones) plus (the number of non-full-length clones), respectively.

Table 5

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequence in the clones isolated from human cDNA libraries constructed by the oligo-capping method, which have the 5'-end sequence that matches a known human mRNA, and also other than those being not full-length according to the comparison with ESTs.			
maximal ATGpr1 score	number of (full-length clones plus non-full-length clones)	number of full-length clones	fullness ratio
>=0.70	9,068	8,349	92.1%
>=0.50	10,345	9,318	90.1%
>=0.30	11,425	9,964	87.2%
>=0.15	12,254	10,335	84.3%
>=0.00	12,785	10,484	82.0%

Table 6

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequence in the clones isolated from human cDNA libraries constructed by the oligo-capping method, which have the 5'-end sequence that matches a known human mRNA, and also other than those being not full-length according to the comparison with ESTs, in which the number of the EST hit is not more than 5.			
maximal ATGpr1 score	number of (full-length clones plus non-full-length clones)	number of full-length clones	fullness ratio
>=0.70	1,959	1,510	77.1%
>=0.50	2,469	1,821	73.8%
>=0.30	2,975	2,046	68.8%
>=0.15	3,368	2,164	64.3%
>=0.00	3,661	2,226	60.8%

[0150] According to the above results, it was found that, in case of using clones isolated from human cDNA libraries constructed by the oligo-capping method, the fullness ratio of the clones that have low score in the ATGpr can be improved by assessing their 5'-end sequence using the combination of the ATGpr and the ESTiMateFL. Therefore, the method was applied to select a cDNA clone with high fullness ratio.

EXAMPLE 4

Clustering of the 5'-end and 3'-end sequences of cDNA clones.

[0151] The 5'-end and 3'-end sequences of cDNA clones were obtained, and clustered separately. Briefly, data of the single pass sequencing of the determined 5'-end and 3'-end of cDNA clones was subjected to the BLAST search between the sequence data of all the clones synthesized in Example 1, and clones that are supposed to be originating from the same gene were clustered into a group. For the 5'-end sequence, those having the consensus sequence of 95% identity 300 base pairs or more are clustered into the same group. For the 3'-end sequence, those having the consensus sequence of 90% identity 200 base pairs or more are clustered into the same group. Among the clusters of the 5'-end and 3'-end sequences, the sequence having the longest lead was chosen as the representative sequence of the cluster (group).

EXAMPLE 5

Characterization of the representative sequences and the sequences of clones

[0152] Data of the 5'-end sequences of the representative sequences and clones was characterized by the following

methods:

(1) judging whether it is identical to the sequence of mRNA or ESTs from human by the BLAST search of the GenBank or SwissProt, and examining whether it is full-length by comparing with the sequences of known mRNA and ESTs from human.
(2) determining the ATGpr1 score using all the initiation codons contained within the 5'-end sequence by the ATGpr which predict fullness ratio.
(3) predicting the existence of the signal sequence using all the initiation codons contained within the 5'-end sequence by the PSORT which predict signal.
and,
(4) only with the 5'-end sequences of the representative sequences of the clusters, examining the keywords in the top hit data of the homology search of the SwissProt.

[0153] Data of the characterized representative sequences and clones was used for the final selection of the clones.

EXAMPLE 6

Identity to the human mRNA and human EST, and comparison of the 5'-end length.

[0154] The clones and the representative sequences of the clusters were judged to be identical to any human mRNA, if their 5'-end sequence has a region of 200 nucleotides or longer with 94% or more identity to the mRNA. The clones and the representative sequences of the clusters were judged to be identical to any human EST, if their 5'-end sequence has a region of 200 nucleotides or longer with 90% or more identity to the EST.

[0155] The clones and the representative sequences of the clusters were judged to be full-length in comparison with human mRNA, if their 5'-end sequence is longer than those of the mRNA, or it contains the translation initiation site. The clones and the representative sequences of the clusters were judged to be full-length in comparison with human EST in the database, if their 5'-end sequence is longer than those of the EST, or even though it is shorter, the difference in length between the two sequences is 50 nucleotides or less, for convenience. Otherwise, the clones and the representative sequences of the clusters were judged to be not full-length.

EXAMPLE 7

Prediction of the fullness ratio by the ATGpr.

[0156] The score in the ATGpr1 is the expectation to be full-length based on calculations, and the higher score reflects the higher fullness ratio as shown in Example 3. Further, the maximal ATGpr1 score represents the score obtained with all the initiation codons contained in the 5'-end sequence of the clones and the representative sequences, and are used for the characterization.

EXAMPLE 8

Prediction of the existence of a signal sequence by the PSORT.

[0157] Prediction of the existence of a signal sequence by the PSORT was performed on all of the amino acid sequences predicted from all the initiation codons in the 5'-end sequence of the clones and the representative sequences of the clusters. By analyzing the presence or absence of the sequence which is predicted to be a signal sequence, which is characteristics of the N-terminus of many secretory proteins, cDNA clones encoding a secretory protein or membrane protein were selected.

EXAMPLE 9

Prediction of the protein function by the BLAST search.

[0158] The 5'-end sequence of the representative sequences of the cluster was analyzed by the BLAST homology search of the SwissProt. The obtained top hit data was classified into those identical to the 5'-end representative sequence (identity was 90% or higher), those not identical to the 5'-end representative sequence (identity was 60% or lower, and compared sequence was not more than 25 nucleotides), and those similar to the 5'-end representative sequence (the rest of the data).

[0159] All the keywords in the SwissProt data corresponding to the top hit data were selected, and the 5'-end representative sequences were classified by the keywords relating with functions.
The keywords relating with a secretory protein or membrane protein are the followings:

growth factor,
cytokine,
hormone,
receptor,
G-protein coupled receptor,
ionic channel,
voltage-gated channel,
calcium channel,
extracellular matrix,
transmembrane, and
signal.

[0160] The keywords relating to glycoprotein is glycoprotein.
[0161] The keywords relating to signal transduction are the followings:

serine/threonine-protein kinase,
tyrosine-protein kinase, and
calmodulin-binding.

[0162] The keywords relating to transcription are the followings:

transcription regulation and activator,
transcription regulation and repressor, and
nuclear protein and repressor.

[0163] The keywords relating to diseases are disease mutation, and syndrome.
[0164] Many keywords overlapped in the respective group (receptor and transmembrane, for example), and some keywords overlapped in different groups (secretory or membrane, and diseases, etc.).

EXAMPLE 10

Selection of clones by characterization.

[0165] From the data obtained by the above characterization, clones encoding a novel secretory protein or membrane protein, or proteins with other predicted functions were selected by the combination of the ATGpr1 score and the prediction of the signal sequence by the PSORT, or according to the top hit data in the homology search of the SwissProt.
[0166] In selecting the clones, the 5'-end sequences that are identical to a human mRNA were ignored, whereas those that are identical to a human mRNA in part but obviously not identical in the other part were included. Because there were clones selected that are identical to a human mRNA in part but obviously not identical in the other part.
[0167] Also, if the finally selected clones were found to be not full-length compared with the sequences of human mRNA and ESTs, these clones were discarded.

EXAMPLE 11

A method for selection of clones by the combination of the ATGpr1 score and the prediction of the signal sequence by the PSORT (a method for selection of secretory proteins and membrane proteins that are novel and full-length).

[0168] The sequences of clones and the representative sequences of their clusters were used to obtain the maximal ATGpr1 score and predict the presence of the signal sequence. First, clones were selected based on the representative sequences of the clusters. The correspondence between the name and SEQ ID of the representative sequences used for selection (Table 368), and the correspondence between the name and SEQ ID of the introns (including the representative sequences of the 5'-end and 3'-end, and ESTs) used for selection of clones from the representative sequences of the groups (Table 369) were shown in the last part of the present specification. Therein, HRIFA and HRIRA indicate the representative sequence of the 5'-end group, and that of the 3'-end group, respectively.

[0169] In the clusters in which a single clone is contained (the sequence of the 5'-end clone = the representative sequence of the 5'-end), selected were the clones that were judged to be full-length in comparison with human mRNA and ESTs, having the maximal ATGpr1 score 0.5 or higher, and predicted to contain the signal sequence, in principle. However, in the following cases, a clone having a longer 5'-end was selected: the maximal ATGpr1 score was less than 0.5, the sequence of the 5'-end was not full-length, the clone was obviously shorter although the clone was not classified into the same cluster according to the BLAST search of the other clones, or the 5'-end sequence corresponding to the 3'-end of the other clones in the same cluster in which the 3'-end sequence of the clone was contained was found to be longer by assembling. Furthermore, if there were multiple full-length clones in the same cluster and it was not successful to determine by assembling which has the longer 5'-end, all the clones were selected. For assembling, the Sequencher(™) (Hitachi Soft Engineering) was used. As a result, the signal sequence predicted to be present in the representative sequence was not present in some of the selected clones. In some cases, the ATGpr1 score became smaller than 0.5 or 0.3. The fullness ratio in these clones was low, yet still it is possible that the clones are full-length. The clones in which the signal sequence predicted to be present in the representative sequence was not present after selection were likely to be without the signal sequence, but still it is possible that the clones encode a membrane protein.

[0170] In the clusters comprising multiple clones, in which the representative sequence of the 5'-end was predicted to contain the signal sequence, selected were the clones having the longest 5'-end sequence among the clones which were judged to be full-length compared with human mRNA and ESTs, having the maximal ATGpr1 score for the 5'-end sequence 0.5 or higher, and predicted to contain the signal sequence. However, in the following cases, a clone having a longer 5'-end was selected: the maximal ATGpr1 score was less than 0.5, the sequence of the 5'-end was not full-length, the clone was obviously shorter although the clone was not classified into the same cluster according to the BLAST search of the other clones, or the 5'-end sequence corresponding to the 3'-end of the other clones in the same cluster in which the 3'-end sequence of the clone was contained was found to be longer. Furthermore, if there were multiple full-length clones in the same cluster and it was not successful to determine by assembling which has the longer 5'-end, all the clones were selected. As a result, the signal sequence predicted to be present in the representative sequence was not present in some of the selected clones. In some cases, the ATGpr1 score became smaller than 0.5 or 0.3. The fullness ratio in these clones was low, yet still it is possible that the clones are full-length. The clones in which the signal sequence predicted to be present in the representative sequence was not present after selection were likely to be without the signal sequence at the 5'-end, but still it is possible that the clones encode a membrane protein.

[0171] Next, in the clusters comprising multiple clones, in which the representative sequence of the 5'-end was predicted to have no signal sequence, selected were the clones which were judged to be full-length compared with human mRNA and ESTs, having the maximal ATGpr1 score for the 5'-end sequence 0.5 or higher, and predicted to contain the signal sequence.

[0172] The number of the clones selected by the combination of the ATGpr1 score and the prediction of a signal sequence by the PSORT were 254. The number of the clones having the maximal ATGpr1 score 0.5 or higher, and predicted to contain a signal sequence were 170 (Table 7-10). Among the clones, 164 clones were found to have the representative sequence of the original cluster that fulfills the same conditions. On the other hand, 5 clones were selected from the representative sequences of the 5'-end of the clusters which was predicted to contain a signal sequence while the maximal ATGpr1 score was lower than 0.5. A clone was selected from the representative sequence of the 5'-end of the cluster which was predicted to have no signal sequence.

[0173] The clones that have the maximal ATGpr1 score 0.3 or higher and less than 0.5 and predicted to contain the signal sequence were 35 clones (Table 11), in which 8 clones were found to have the representative sequence of the original cluster that fulfills the same conditions. Twenty-seven clones were selected from the representative sequences of the clusters which have the maximal ATGpr1 score 0.5 or higher and were predicted to have no signal sequence.

[0174] The clones that have the maximal ATGpr1 score less than 0.3 and were predicted to contain a signal sequence were 41 clones (Table 12). The clones that have the maximal ATGpr1 score 0.5 or higher and were predicted to have no signal sequence were 4 clones (Table 13). The clones that have the maximal ATGpr1 score 0.3 or higher and less than 0.5 and were predicted to have no signal sequence were 2 clones (Table 14). The clones that have the maximal ATGpr1 score less than 0.3 and were predicted to contain a signal sequence were 2 clones (Table 15). The representative sequences of the original clusters of all the clones had the maximal ATGpr1 score 0.3 or higher, and were predicted to contain a signal sequence.

[0175] The fullness ratio of the clones having the maximal ATGpr1 score 0.5 or higher, 0.3 or higher, and 0 or higher is expected to be as shown in Table 3, 4, 5, and 6.

Table 7

The 170 clones in which the selected clones have the maximal ATGpr1 score 0.5 or higjer, and were predicted to contain a signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	name of representative sequence	maximal ATGpr1 score	signal
HEMBA1000713	F-HEMBA1000713	0.67	Yes	HRIFA017729a	0.57	Yes
HEMBA1000962	F-HEMBA1000962	0.69	Yes	HRIFA000899a	0.69	Yes
HEMBA1001272	F-HEMBA1001272	0.94	Yes	HRIFA001179a	0.94	Yes
HEMBA1001297	F-HEMBA1001297	0.89	Yes	HRIFA001201a	0.89	Yes
HEMBA1002420	F-HEMBA1002420	0.6	Yes	HRIFA002195a	0.6	Yes
HEMBA1003101	F-HEMBA1003101	0.67	Yes	HRIFA002787a	0.94	Yes
HEMBA1003399	F-HEMBA1003399	0.94	Yes	HRIFA002985a	0.94	Yes
HEMBA1003732	F-HEMBA1003732	0.86	Yes	HRIFA003169a	0.86	Yes
HEMBA1004110	F-HEMBA1004110	0.59	Yes	HRIFA003379a	0.59	Yes
HEMBA1005430	F-HEMBA1005430	0.69	Yes	HRIFA020661a	0.69	Yes
HEMBA1006016	F-HEMBA1006016	0.6	Yes	HRIFA020466a	0.6	Yes
HEMBA1006171	F-HEMBA1006171	0.62	Yes	HRIFA021399a	0.62	Yes
HEMBA1006311	F-HEMBA1006311	0.94	Yes	HRIFA021594a	0.94	Yes
HEMBA1006335	F-HEMBA1006335	0.83	Yes	HRIFA012069a	0.94	Yes
HEMBA1006357	F-HEMBA1006357	0.67	Yes	HRIFA021448a	0.67	Yes
HEMBA1006658	F-HEMBA1006658	0.66	Yes	HRIFA021323a	0.66	Yes
HEMBA1006707	F-HEMBA1006707	0.66	Yes	HRIFA021499a	0.94	Yes
HEMBA1006902	F-HEMBA1006902	0.66	Yes	HRIFA021754a	0.94	Yes
HEMBA1006960	F-HEMBA1006960	0.94	Yes	HRIFA021886a	0.94	Yes
HEMBB1000276	F-HEMBB1000276	0.94	Yes	HRIFA029577a	0.94	Yes
HEMBB1000642	F-HEMBB1000642	0.94	Yes	HRIFA029779a	0.94	Yes
HEMBB1000905	F-HEMBB1000905	0.94	Yes	HRIFA009764a	0.91	Yes
HEMBB1001200	F-HEMBB1001200	0.83	Yes	HRIFA030839a	0.81	Yes
HEMBB1001407	F-HEMBB1001407	0.87	Yes	HRIFA030981a	0.87	Yes
HEMBB1001530	F-HEMBB1001530	0.6	Yes	HRIFA031062a	0.6	Yes
HEMBB1001547	F-HEMBB1001547	0.87	Yes	HRIFA031075a	0.87	Yes
HEMBB1001978	F-HEMBB1001978	0.7	Yes	HRIFA031350a	0.7	Yes
HEMBB1002162	F-HEMBB1002162	0.91	Yes	HRIFA031472a	0.91	Yes
HEMBB1002228	F-HEMBB1002228	0.53	Yes	HRIFA031510a	0.53	Yes
HEMBB1002245	F-HEMBB1002245	0.94	Yes	HRIFA032984a	0.94	Yes
HEMBB1002427	F-HEMBB1002427	0.57	Yes	HRIFA005760a	0.94	Yes
HEMBB1002465	F-HEMBB1002465	0.72	Yes	HRIFA031672a	0.72	Yes
HEMBB1002693	F-HEMBB1002693	0.64	Yes	HRIFA031895a	0.64	Yes
MAMMA1000046	F-MAMMA1000046	0.7	Yes	HRIFA024841a	0.7	Yes
MAMMA1000102	F-MAMMA1000102	0.79	Yes	HRIFA026151a	0.79	Yes
MAMMA1000118	F-MAMMA1000118	0.81	Yes	HRIFA026153a	0.81	Yes
MAMMA1000141	F-MAMMA1000141	0.8	Yes	HRIFA024554a	0.8	Yes
MAMMA1000449	F-MAMMA1000449	0.94	Yes	HRIFA026203a	0.94	Yes
MAMMA1000457	F-MAMMA1000457	0.78	Yes	HRIFA026210a	0.78	Yes
MAMMA1000652	F-MAMMA1000652	0.94	Yes	HRIFA026346a	0.94	Yes
MAMMA1000994	F-MAMMA1000994	0.84	Yes	HRIFA026735a	0.84	Yes
MAMMA1001141	F-MAMMA1001141	0.89	Yes	HRIFA027265a	0.89	Yes
MAMMA1001310	F-MAMMA1001310	0.74	Yes	HRIFA026899a	0.74	Yes
MAMMA1001344	F-MAMMA1001344	0.71	Yes	HRIFA026918a	0.71	Yes
MAMMA1002070	F-MAMMA1002070	0.6	Yes	HRIFA028371a	0.82	Yes
MAMMA1002087	F-MAMMA1002087	0.68	Yes	HRIFA027619a	0.68	Yes
MAMMA1002165	F-MAMMA1002165	0.57	Yes	HRIFA027673a	0.34	Yes
MAMMA1002205	F-MAMMA1002205	0.74	Yes	HRIFA027701a	0.74	Yes
MAMMA1002633	F-MAMMA1002633	0.53	Yes	HRIFA030461a	0.94	Yes
NT2RM2000241	F-NT2RM2000241	0.94	Yes	HRIFA020965a	0.94	Yes
NT2RM2000514	F-NT2RM2000514	0.51	Yes	HRIFA022106a	0.51	Yes
NT2RM2001643	F-NT2RM2001643	0.69	Yes	HRIFA028926a	0.69	Yes
NT2RM4000115	F-NT2RM4000115	0.56	Yes	HRIFA025792a	0.53	Yes
NT2RM4000997	F-NT2RM4000997	0.94	Yes	HRIFA029274a	0.94	Yes

1/4 (continued)

Table 8

The 170 clones in which the selected clones have the maximal ATGpr1 score 0.5 or higher, and were predicted to contain the signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	name of representative sequence	maximal ATGpr1 score	signal
NT2RM4001321	F-NT2RM4001321	0.74	Yes	HRIFA024533a	0.74	Yes
NT2RM4001325	F-NT2RM4001325	0.94	Yes	HRIFA033349a	0.94	Yes
NT2RM4001768	F-NT2RM4001768	0.73	Yes	HRIFA013668a	0.5	Yes
NT2RP1000448	F-NT2RP1000448	0.62	Yes	HRIFA005356a	0.62	Yes
NT2RP1001563	F-NT2RP1001563	0.52	Yes	HRIFA006018a	0.52	Yes
NT2RP2001915	F-NT2RP2001915	0.94	Yes	HRIFA007541a	0.94	Yes
NT2RP2002015	F-NT2RP2002015	0.94	Yes	HRIFA007619a	0.94	Yes
NT2RP2002063	F-NT2RP2002063	0.87	Yes	HRIFA007659a	0.94	Yes
NT2RP2002304	F-NT2RP2002304	0.87	Yes	HRIFA007829a	0.94	Yes
NT2RP2002674	F-NT2RP2002674	0.8	Yes	HRIFA008099a	0.8	Yes
NT2RP2002721	F-NT2RP2002721	0.56	Yes	HRIFA008131a	0.56	Yes
NT2RP2003383	F-NT2RP2003383	0.67	Yes	HRIFA008606a	0.67	Yes
NT2RP2003593	F-NT2RP2003593	0.73	Yes	HRIFA008252a	0.94	Yes
NT2RP2003599	F-NT2RP2003599	0.58	Yes	HRIFA008753a	0.58	Yes
NT2RP2003655	F-NT2RP2003655	0.78	Yes	HRIFA008784a	0.83	Yes
NT2RP2004179	F-NT2RP2004179	0.83	Yes	HRIFA008827a	0.83	Yes
NT2RP2004495	F-NT2RP2004495	0.58	Yes	HRIFA009372a	0.58	Yes
NT2RP2004524	F-NT2RP2004524	0.73	Yes	HRIFA009392a	0.82	Yes
NT2RP2004556	F-NT2RP2004556	0.81	Yes	HRIFA009414a	0.81	Yes
NT2RP2004837	F-NT2RP2004837	0.94	Yes	HRIFA006216a	0.93	Yes
NT2RP2005027	F-NT2RP2005027	0.92	Yes	HRIFA004145a	0.93	Yes
NT2RP2005463	F-NT2RP2005463	0.93	Yes	HRIFA010034a	0.42	No
NT2RP2005514	F-NT2RP2005514	0.58	Yes	HRIFA010070a	0.58	Yes
NT2RP2005887	F-NT2RP2005887	0.94	Yes	HRIFA010322a	0.94	Yes
NT2RP2006269	F-NT2RP2006269	0.78	Yes	HRIFA025913a	0.57	Yes
NT2RP3000169	F-NT2RP3000169	0.94	Yes	HRIFA022262a	0.94	Yes
NT2RP3000460	F-NT2RP3000460	0.61	Yes	HRIFA022794a	0.61	Yes
NT2RP3000789	F-NT2RP3000789	0.62	Yes	HRIFA023605a	0.62	Yes
NT2RP3000818	F-NT2RP3000818	0.52	Yes	HRIFA023619a	0.52	Yes
NT2RP3001012	F-NT2RP3001012	0.67	Yes	HRIFA023129a	0.22	Yes
NT2RP3001044	F-NT2RP3001044	0.93	Yes	HRIFA007026a	0.73	Yes
NT2RP3001560	F-NT2RP3001560	0.58	Yes	HRIFA030599a	0.92	Yes
NT2RP3001685	F-NT2RP3001685	0.5	Yes	HRIFA023521a	0.5	Yes
NT2RP3001858	F-NT2RP3001858	0.94	Yes	HRIFA026490a	0.94	Yes
NT2RP3002160	F-NT2RP3002160	0.61	Yes	HRIFA005760a	0.94	Yes
NT2RP3002836	F-NT2RP3002836	0.68	Yes	HRIFA024392a	0.72	Yes
NT2RP3002958	F-NT2RP3002958	0.54	Yes	HRIFA017670a	0.91	Yes
NT2RP3003535	F-NT2RP3003535	0.94	Yes	HRIFA025498a	0.94	Yes
NT2RP3004000	F-NT2RP3004000	0.93	Yes	HRIFA025276a	0.93	Yes
NT2RP3004321	F-NT2RP3004321	0.81	Yes	HRIFA025786a	0.81	Yes
NT2RP3004355	F-NT2RP3004355	0.6	Yes	HRIFA025360a	0.6	Yes
NT2RP3004374	F-NT2RP3004374	0.58	Yes	HRIFA024533a	0.74	Yes
NT2RP4001001	F-NT2RP4001001	0.53	Yes	HRIFA009214a	0.5	Yes
NT2RP4002715	F-NT2RP4002715	0.94	Yes	HRIFA024921a	0.53	Yes
OVARC1000298	F-OVARC1000298	0.61	Yes	HRIFA004852a	0.59	Yes
OVARC1000775	F-OVARC1000775	0.7	Yes	HRIFA011347a	0.7	Yes
OVARC1000811	F-OVARC1000811	0.52	Yes	HRIFA000974a	0.39	Yes
OVARC1000853	F-OVARC1000853	0.94	Yes	HRIFA011403a	0.94	Yes
OVARC1001222	F-OVARC1001222	0.79	Yes	HRIFA022714a	0.67	Yes
OVARC1001807	F-OVARC1001807	0.52	Yes	HRIFA021069a	0.52	Yes
OVARC1001833	F-OVARC1001833	0.9	Yes	HRIFA021136a	0.9	Yes
PLACE1000231	F-PLACE1000231	0.52	Yes	HRIFA011802a	0.52	Yes
PLACE1000560	F-PLACE1000560	0.88	Yes	HRIFA012022a	0.88	Yes
PLACE1000740	F-PLACE1000740	0.57	Yes	HRIFA012151a	0.57	Yes

2/4 (continued)

Table 9

The 170 clones in which the selected clones have the maximal ATGpr1 score 0.5 or higher, and were predicted to contain the signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	name of representative sequence	maximal ATGpr1 score	signal
PLACE1000912	F-PLACE1000912	0.9	Yes	HRIFA012282a	0.9	Yes
PLACE1000914	F-PLACE1000914	0.94	Yes	HRIFA012283a	0.94	Yes
PLACE1000927	F-PLACE1000927	0.71	Yes	HRIFA012290a	0.71	Yes
PLACE1000986	F-PLACE1000986	0.51	Yes	HRIFA012333a	0.51	Yes
PLACE1001100	F-PLACE1001100	0.76	Yes	HRIFA012417a	0.76	Yes
PLACE1001183	F-PLACE1001183	0.69	Yes	HRIFA012480a	0.69	Yes
PLACE1001229	F-PLACE1001229	0.65	Yes	HRIFA012513a	0.65	Yes
PLACE1001407	F-PLACE1001407	0.83	Yes	HRIFA012069a	0.94	Yes
PLACE1001788	F-PLACE1001788	0.6	Yes	HRIFA012881a	0.6	Yes
PLACE1002374	F-PLACE1002374	0.68	Yes	HRIFA013265a	0.92	Yes
PLACE1002518	F-PLACE1002518	0.94	Yes	HRIFA018849a	0.78	Yes
PLACE1003839	F-PLACE1003839	0.67	Yes	HRIFA014178a	0.6	Yes
PLACE1003845	F-PLACE1003845	0.92	Yes	HRIFA019185a	0.92	Yes
PLACE1004199	F-PLACE1004199	0.94	Yes	HRIFA014417a	0.94	Yes
PLACE1004282	F-PLACE1004282	0.94	Yes	HRIFA014467a	0.94	Yes
PLACE1004305	F-PLACE1004305	0.87	Yes	HRIFA014482a	0.87	Yes
PLACE1004637	F-PLACE1004637	0.89	Yes	HRIFA014692a	0.89	Yes
PLACE1005005	F-PLACE1005005	0.55	Yes	HRIFA014953a	0.55	Yes
PLACE1005250	F-PLACE1005250	0.52	Yes	HRIFA015129a	0.52	Yes
PLACE1005410	F-PLACE1005410	0.61	Yes	HRIFA015236a	0.61	Yes
PLACE1005725	F-PLACE1005725	0.92	Yes	HRIFA015443a	0.92	Yes
PLACE1005768	F-PLACE1005768	0.62	Yes	HRIFA015471a	0.62	Yes
PLACE1005927	F-PLACE1005927	0.66	Yes	HRIFA015568a	0.94	Yes
PLACE1006079	F-PLACE1006079	0.56	Yes	HRIFA015671a	0.56	Yes
PLACE1006093	F-PLACE1006093	0.59	Yes	HRIFA015682a	0.59	Yes
PLACE1006219	F-PLACE1006219	0.94	Yes	HRIFA015764a	0.93	Yes
PLACE1006809	F-PLACE1006809	0.66	Yes	HRIFA016129a	0.66	Yes
PLACE1007040	F-PLACE1007040	0.87	Yes	HRIFA013288a	0.87	Yes
PLACE1007096	F-PLACE1007096	0.59	Yes	HRIFA012167a	0.82	Yes
PLACE1007626	F-PLACE1007626	0.67	Yes	HRIFA016623a	0.67	Yes
PLACE1007971	F-PLACE1007971	0.74	Yes	HRIFA016838a	0.74	Yes
PLACE1008985	F-PLACE1008985	0.65	Yes	HRIFA017457a	0.48	Yes
PLACE1009067	F-PLACE1009067	0.59	Yes	HRIFA017509a	0.59	Yes
PLACE1009196	F-PLACE1009196	0.73	Yes	HRIFA017594a	0.73	Yes
PLACE1009527	F-PLACE1009527	0.58	Yes	HRIFA017791a	0.87	Yes
PLACE1009982	F-PLACE1009982	0.94	Yes	HRIFA018075a	0.94	Yes
PLACE1011236	F-PLACE1011236	0.52	Yes	HRIFA018827a	0.66	Yes
PLACE2000219	F-PLACE2000219	0.73	Yes	HRIFA034010a	0.73	Yes
SKNMC1000004	F-SKNMC1000004	0.94	Yes	HRIFA030097a	0.94	Yes
THYRO1000036	F-THYRO1000036	0.83	Yes	HRIFA027754a	0.83	Yes
THYRO1000099	F-THYRO1000099	0.94	Yes	HRIFA027803a	0.94	Yes
THYRO1001237	F-THYRO1001237	0.94	Yes	HRIFA030248a	0.94	Yes
THYRO1001327	F-THYRO1001327	0.93	Yes	HRIFA025125a	0.94	Yes
THYRO1001495	F-THYRO1001495	0.89	Yes	HRIFA030394a	0.89	Yes
THYRO1001523	F-THYRO1001523	0.71	Yes	HRIFA030408a	0.71	Yes
THYRO1001725	F-THYRO1001725	0.94	Yes	HRIFA029107a	0.94	Yes
Y79AA1000226	F-Y79AA1000226	0.94	Yes	HRIFA027874a	0.94	Yes
Y79AA1000521	F-Y79AA1000521	0.92	Yes	HRIFA027961a	0.92	Yes
Y79AA1000775	F-Y79AA1000776	0.78	Yes	HRIFA028401a	0.78	Yes
Y79AA1000959	F-Y79AA1000959	0.9	Yes	HRIFA028465a	0.9	Yes
Y79AA1001013	F-Y79AA1001013	0.94	Yes	HRIFA011193a	0.94	Yes
Y79AA1001264	F-Y79AA1001264	0.94	Yes	HRIFA028573a	0.94	Yes
Y79AA1001328	F-Y79AA1001328	0.91	Yes	HRIFA028592a	0.91	Yes
Y79AA1001427	F-Y79AA1001427	0.65	Yes	HRIFA028652a	0.65	Yes

3/4 (continued)

Table 10

The 170 clones in which the selected clones have the maximal ATGpr1 score 0.5 or higher, and were predicted to contain the signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	name of representative sequence	maximal ATGpr1 score	signal
Y79AA1001430	F-Y79AA1001430	0.94	Yes	HRIFA028654a	0.94	Yes
Y79AA1001530	F-Y79AA1001530	0.94	Yes	HRIFA010206a	0.94	Yes
Y79AA1001592	F-Y79AA1001592	0.94	Yes	HRIFA028708a	0.94	Yes
Y79AA1001793	F-Y79AA1001793	0.89	Yes	HRIFA032066a	0.89	Yes
Y79AA1001795	F-Y79AA1001795	0.59	Yes	HRIFA032067a	0.59	Yes
Y79AA1001863	F-Y79AA1001863	0.56	Yes	HRIFA032097a	0.15	Yes
Y79AA1002022	F-Y79AA1002022	0.94	Yes	HRIFA033718a	0.94	Yes
Y79AA1002373	F-Y79AA1002373	0.79	Yes	HRIFA032271a	0.79	Yes

Table 11

The 35 clones in which the selected clones have the maximal ATGpr1 score 0.3 or higher and less than 0.5, and were predicted to contain the signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	representative sequence	maximal ATGpr1 score	signal
HEMBA1000907	F-HEMBA1000907	0.39	Yes	HRIFA000845a	0.94	Yes
HEMBA1003602	F-HEMBA1003602	0.43	Yes	HRIFA020109a	0.43	Yes
HEMBA1004797	F-HEMBA1004797	0.45	Yes	HRIFA020883a	0.66	Yes
HEMBB1000447	F-HEMBB1000447	0.31	Yes	HRIFA001558a	0.76	Yes
MAMMA1000591	F-MAMMA1000591	0.34	Yes	HRIFA026303a	0.77	Yes
MAMMA1000681	F-MAMMA1000681	0.35	Yes	HRIFA026364a	0.94	Yes
MAMMA1000986	F-MAMMA1000986	0.37	Yes	HRIFA021611a	0.37	Yes
MAMMA1001893	F-MAMMA1001893	0.44	Yes	HRIFA027485a	0.9	Yes
MAMMA1001957	F-MAMMA1001957	0.48	Yes	HRIFA027536a	0.94	Yes
NT2RM2001941	F-NT2RM2001941	0.44	Yes	HRIFA032011a	0.94	Yes
NT2RP1000050	F-NT2RP1000050	0.47	Yes	HRIFA005102a	0.54	Yes
NT2RP1000903	F-NT2RP1000903	0.38	Yes	HRIFA005650a	0.38	Yes
NT2RP2003469	F-NT2RP2003469	0.33	Yes	HRIFA008661a	0.9	Yes
NT2RP2003664	F-NT2RP2003664	0.36	Yes	HRIFA008790a	0.89	Yes
NT2RP2004447	F-NT2RP2004447	0.36	Yes	HRIFA009339a	0.93	Yes
NT2RP2006042	F-NT2RP2006042	0.37	Yes	HRIFA010425a	0.69	Yes
NT2RP3001195	F-NT2RP3001195	0.44	Yes	HRIFA023227a	0.94	Yes
NT2RP3003354	F-NT2RP3003354	0.3	Yes	HRIFA008212a	0.51	Yes
NT2RP3003469	F-NT2RP3003469	0.3	Yes	HRIFA025143a	0.3	Yes
NT2RP3003963	F-NT2RP3003963	0.44	Yes	HRIFA008949a	0.62	Yes
NT2RP3004133	F-NT2RP3004133	0.35	Yes	HRIFA025706a	0.94	Yes
NT2RP3004309	F-NT2RP3004309	0.4	Yes	HRIFA025778a	0.92	Yes
OVARC1000208	F-OVARC1000208	0.4	Yes	HRIFA010942a	0.4	Yes
PLACE1001536	F-PLACE1001536	0.33	Yes	HRIFA012761a	0.31	Yes
PLACE1003407	F-PLACE1003407	0.48	Yes	HRIFA013899a	0.48	Yes
PLACE1003428	F-PLACE1003428	0.37	Yes	HRIFA013911a	0.61	Yes
PLACE1003460	F-PLACE1003460	0.38	Yes	HRIFA013932a	0.94	Yes
PLACE1005569	F-PLACE1005569	0.32	Yes	HRIFA015351a	0.68	Yes
PLACE1006277	F-PLACE1006277	0.32	Yes	HRIFA015802a	0.65	Yes
PLACE1010251	F-PLACE1010251	0.32	Yes	HRIFA018238a	0.62	Yes
THYRO1000196	F-THYRO1000196	0.44	Yes	HRIFA029050a	0.71	Yes
THYRO1000795	F-THYRO1000795	0.33	Yes	HRIFA029327a	0.92	Yes
THYRO1000999	F-THYRO1000999	0.4	Yes	HRIFA030203a	0.4	Yes
THYRO1001478	F-THYRO1001478	0.47	Yes	HRIFA030385a	0.89	Yes
Y79AA1000426	F-Y79AA1000426	0.47	Yes	HRIFA027940a	0.92	Yes

Table 12

41 clones from which selected clones have the maximal ATGpr1 score 0 or higher and less than 0.3, and predicted to be containing the signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	representative sequence	maximal ATGpr1 score	signal
HEMBA1000300	F-HEMBA1000300	0.13	Yes	HRIFA000284a	0.13	Yes
HEMBA1002164	F-HEMBA1002164	0.11	Yes	HRIFA001972a	0.74	Yes
HEMBA1002239	F-HEMBA1002239	0.17	Yes	HRIFA002037a	0.17	Yes
HEMBA1002421	F-HEMBA1002421	0.22	Yes	HRIFA005392a	0.9	Yes
HEMBA1003294	F-HEMBA1003294	0.15	Yes	HRIFA020163a	0.15	Yes
HEMBA1006572	F-HEMBA1006572	0.06	Yes	HRIFA021543a	0.62	Yes
HEMBA1007013	F-HEMBA1007013	0.19	Yes	HRIFA021906a	0.82	Yes
HEMBB1000567	F-HEMBB1000567	0.09	Yes	HRIFA029730a	0.15	Yes
HEMBB1002663	F-HEMBB1002663	0.29	Yes	HRIFA031871a	0.29	Yes
MAMMA1001043	F-MAMMA1001043	0.17	Yes	HRIFA026764a	0.81	Yes
MAMMA1001284	F-MAMMA1001284	0.26	Yes	HRIFA026889a	0.26	Yes
MAMMA1001901	F-MAMMA1001901	0.17	Yes	HRIFA027493a	0.17	Yes
MAMMA1002224	F-MAMMA1002224	0.13	Yes	HRIFA027717a	0.13	Yes
NT2RM2000306	F-NT2RM2000306	0.25	Yes	HRIFA021985a	0.25	Yes
NT2RM2000410	F-NT2RM2000410	0.22	Yes	HRIFA022055a	0.82	Yes
NT2RP2000479	F-NT2RP2000479	0.24	Yes	HRIFA000822a	0.12	Yes
NT2RP2001495	F-NT2RP2001495	0.19	Yes	HRIFA007228a	0.78	Yes
NT2RP2001948	F-NT2RP2001948	0.29	Yes	HRIFA007565a	0.89	Yes
NT2RP3000645	F-NT2RP3000645	0.2	Yes	HRIFA022890a	0.91	Yes
NT2RP3003076	F-NT2RP3003076	0.23	Yes	HRIFA024978a	0.65	Yes
NT2RP4001879	F-NT2RP4001879	0.26	Yes	HRIFA017818a	0.79	Yes
NT2RP4002451	F-NT2RP4002451	0.11	Yes	HRIFA018447a	0.34	Yes
OVARC1000439	F-OVARC1000439	0.15	Yes	HRIFA011105a	0.21	Yes
OVARC1001727	F-OVARC1001727	0.22	Yes	HRIFA019960a	0.22	Yes
PLACE1002080	F-PLACE1002080	0.17	Yes	HRIFA013092a	0.76	Yes
PLACE1002095	F-PLACE1002095	0.23	Yes	HRIFA013103a	0.61	Yes
PLACE1004028	F-PLACE1004028	0.12	Yes	HRIFA014303a	0.12	Yes
PLACE1004482	F-PLACE1004482	0.13	Yes	HRIFA014590a	0.57	Yes
PLACE1005383	F-PLACE1005383	0.11	Yes	HRIFA015219a	0.52	Yes
PLACE1005544	F-PLACE1005544	0.08	Yes	HRIFA009852a	0.41	Yes
PLACE1005660	F-PLACE1005660	0.2	Yes	HRIFA015409a	0.2	Yes
PLACE1006443	F-PLACE1006443	0.27	Yes	HRIFA015902a	0.89	Yes
PLACE1007296	F-PLACE1007296	0.22	Yes	HRIFA016430a	0.27	Yes
PLACE1008469	F-PLACE1008469	0.27	Yes	HRIFA017146a	0.94	Yes
PLACE1008984	F-PLACE1008984	0.11	Yes	HRIFA017456a	0.74	Yes
PLACE4000455	F-PLACE4000455	0.23	Yes	HRIFA012333a	0.51	Yes
SKNMC1000014	F-SKNMC1000014	0.15	Yes	HRIFA030106a	0.76	Yes
THYRO1001702	F-THYRO1001702	0.14	Yes	HRIFA030511a	0.8	Yes
Y79AA1000270	F-Y79AA1000270	0.21	Yes	HRIFA005644a	0.63	Yes
Y79AA1001056	F-Y79AA1001056	0.27	Yes	HRIFA028497a	0.27	Yes
Y79AA1001803	F-Y79AA1001803	0.08	Yes	HRIFA032073a	0.68	Yes

Table 13

Four clones from which selected clones have the maximal ATGpr1 score 0.5 or higher, and predicted to be lacking the signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	name of representative sequence	maximal ATGpr1 score	signal
NT2RP3002281	F-NT2RP3002281	0.81	No	HRIFA012999a	0.61	Yes
NT2RP3002721	F-NT2RP3002721	0.94	No	HRIFA023305a	0.57	Yes
NT2RP3004083	F-NT2RP3004083	0.94	No	HRIFA008387a	0.76	Yes
PLACE1005669	F-PLACE1005669	0.94	No	HRIFA012513a	0.65	Yes

Table 14

Two clones from which selected clones have the maximal ATGpr1 score 0.3 or higher and less than 0.5 and predicted to have no signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	representative sequence	maximal ATGpr1 score	signal
NT2RP3000481	F-NT2RP3000481	0.47	No	HRIFA028614a	0.93	Yes
NT2RP3003559	F-NT2RP3003559	0.48	No	HRIFA025514a	0.45	Yes

Table 15

Two clones from which selected clones have the maximal ATGpr1 score 0 or higher and less than 0.3, and predicted to have no signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	representative sequence	maximal ATGpr1 score	signal
PLACE1005601	F-PLACE1005601	0.12	No	HRIFA010593a	0.64	Yes
PLACE1006786	F-PLACE1006786	0.22	No	HRIFA012333a	0.51	Yes

EXAMPLE 12

A method for the selection of clones based on the top hit data in the homology search against the SwissProt (a method for the selection of a novel full-length protein that is predicted to have a function based on the top hit data).

[0176] The representative sequences of the clusters were discarded in which the 5'-end sequence is identical (90% or more matching), or not similar (the compared part contains a sequence of 25 nucleotides or shorter and the similarity is lower than 60%) to the top hit data in the SwissProt. Then, the remaining representative sequences which has similarity to the representative sequences of the 5'-ends were classified by a group of the above keywords (some representative sequences belong to a group by multiple keywords), and then clones were selected from the clusters. The names and the corresponding SEQ IDs of the representative sequences, and also the names of the introns (including the representative sequence of the 5'-end or the 3'-end, or ESTs) used for selecting the clones from the representative sequences and the corresponding SEQ IDs are shown in the last part of the present specification (Table 368 and 369, respectively). HRIFA indicates the representative sequence of the 5'-end group, and HRIRA indicates the representative sequence of the 3'-end group.

[0177] In principle, from the clusters containing only a single clone (the 5'-end sequence is the representative sequence of the cluster), the clone was selected. However, in the following cases, the clone containing a longer 5'-end was selected: where the maximal ATGpr1 score was less than 0.5, the 5'-end sequence of the clone to be selected was not complete, or the 5'-end of the clone was found to be obviously short nevertheless the clone should not be

included in the same cluster based on the BLAST analysis between the other clones, or further, the 5'-end sequence of the said clone, which corresponds to the 3'-ends of the other clones belonging to the same cluster in which the 3'-end of the said clone was included, was turn out to be longer than those of the other clones by assembling them. When there were two clones in the same cluster, judged to be full-length, and it was difficult to determine which clone has the longer 5'-end even by assembling them, all the clones were selected. As a result, the ATGpr1 score in some clones became less than 0.5 or less than 0.3. The fullness ratio of these clones became lower, but there is still a possibility that the clones are full-length.

[0178] In the case in which multiple clones were contained in a cluster, selected was the clone having the longest 5'-end in the clones judged to be full-length compared to the human mRNA or human EST. However, in the following cases, the clone containing a longer 5'-end was selected: where the maximal ATGpr1 score was less than 0.5, the 5'-end sequence of the clone to be selected was not complete, or the 5'-end of the clone was found to be obviously short nevertheless the clone should not be included in the same cluster based on the BLAST analysis between the other clones, or further, the 5'-end sequence of the said clone, which corresponds to the 3'-ends of the other clones belonging to the same cluster in which the 3'-end of the said clone was included, was turn out to be longer than those of the other clones by assembling them. When there were two clones in the same cluster, judged to be full-length, and it was difficult to determine which clone has the longer 5'-end even by assembling them, all the clones were selected. As a result, the ATGpr1 score in some clones became less than 0.5 or less than 0.3. These clones can still be full-length.

[0179] Based on the top hit data in the SwissProt homology search, 658 clones were selected. Among them, 446 clones were selected by the keywords, secretion or membrane. Using the keyword, glycoprotein, 243 clones were selected. 51 clones were selected by the keywords for signal transduction. With the keywords for transcription, 130 clones were selected. 17 clones were selected by the keywords for disease.

[0180] Among the 446 clones selected by the keywords, secretion or membrane, 77 clones were overlapped with those selected by combining the ATGpr1 score and prediction by the PSORT for the existence of a signal sequence. Also, many clones were overlapped with those selected by the keyword, glycoprotein. Moreover, some clones were overlapped with the clones selected by the keywords for diseases.

[0181] Among the 243 clones selected by the keyword, glycoprotein, 53 clones were overlapped with those selected by combining the ATGpr1 score and prediction by the PSORT for the existence of a signal sequence. Also, many clones were overlapped with those selected by the keywords, secretion or membrane. Moreover, some clones were overlapped with the clones selected by the keywords in diseases.

[0182] Among the clones selected by the top hit data in the homology search on the SwissProt, 532 clones were having the maximal ATGpr1 score 0.5 or higher. 59 clones were having the maximal score 0.3 or higher and less than 0.5. 67 clones were with the maximal score less than 0.3.

[0183] When the maximal ATGpr1 score is 0.5 or higher, 0.3 or higher, no less than 0, the expected fullness ratio is as shown in Table 3, 4, 5, and 6, respectively.

Table 16

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "growth factor", "cytokine", or "hormone", and the selected clones.

name of clone	name of representative sequence
HEMBA1001563	HRIFA001439a
HEMBA1003047	HRIFA002743a
HEMBA1005070	HRIFA020144a
HEMBA1006724	HRIFA021620a
HEMBA1006916	HRIFA021855a
MAMMA1001066	HRIFA027355a
MAMMA1001634	HRIFA027187a
MAMMA1002165	HRIFA027673a
NT2RM4000326	HRIFA032530a
NT2RM4001377	HRIFA005300a
NT2RP2000447	HRIFA006448a
NT2RP2000663	HRIFA006609a
NT2RP2000903	HRIFA006798a
NT2RP2002974	HRIFA027860a
NT2RP2003369	HRIFA008596a
NT2RP2004141	HRIFA009123a

Table 16 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "growth factor", "cytokine", or "hormone", and the selected clones.	
name of clone	name of representative sequence
NT2RP2005941	HRIFA010361a
NT2RP2006099	HRIFA010466a
NT2RP3000645	HRIFA022890a
NT2RP3000838	HRIFA005300a
NT2RP4002451	HRIFA018447a
OVARC1000275	HRIFA010988a
OVARC1001030	HRIFA021061a
PLACE1004492	HRIFA014598a
PLACE1009279	HRIFA017643a
THYRO1001071	HRIFA029440a
Y79AA1000207	HRIFA027867a
Y79AA1000426	HRIFA027940a

Table 17

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "receptor", "G-protein coupled receptor", "ionic channel", "voltage-gated channel", or "calcium channel", and the selected clones.	
name of clone	name of representative sequence
BNGH41000091	HRIFA029511a
HEMBA1001621	HRIFA001489a
HEMBA1003392	HRIFA002980a
HEMBA1005545	HRIFA020272a
HEMBA1007291	HRIFA022462a
HEMBA1007332	HRIFA022493a
MAMMA1000681	HRIFA026364a
MAMMA1000706	HRIFA026382a
MAMMA 1001978	HRIFA027549a
NT2RM2001939	HRIFA032009a
NT2RM2001941	HRIFA032011a
NT2RM4002352	HRIFA001337a
NT2RP2002510	HRIFA007985a
NT2RP2002533	HRIFA008000a
NT2RP2005181	HRIFA005409a
NT2RP3000304	HRIFA022616a
NT2RP3001542	HRIFA028501a
NT2RP3002409	HRIFA024197a
NT2RP3002836	HRIFA024392a
NT2RP3003000	HRIFA024767a
NT2RP3004552	HRIFA025904a
NT2RP4001877	HRIFA032433a
NT2RP4002750	HRIFA028157a
OVARC1000090	HRIFA010859a
OVARC1000956	HRIFA011484a
OVARC1001991	HRIFA019498a
PLACE1001016	HRIFA012354a
PLACE1001340	HRIFA012584a

Table 17 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "receptor", "G-protein coupled receptor", "ionic channel", "voltage-gated channel", or "calcium channel", and the selected clones.	
name of clone	name of representative sequence
PLACE1001401	HRIFA012625a
PLACE 1001564	HRIFA012737a
PLACE1001655	HRIFA012795a
PLACE 1002547	HRIFA013376a
PLACE 1002967	HRIFA013620a
PLACE 1003573	HRIFA014006a
PLACE1003852	HRIFA014185a
PLACE1004441	HRIFA014561a
PLACE1005031	HRIFA014967a
PLACE1005878	HRIFA015536a
PLACE1007296	HRIFA016430a
PLACE 1008469	HRIFA017146a
PLACE1010784	HRIFA031126a
PLACE1010968	HRIFA018666a
THYRO1000956	HRIFA029393a
Y79AA1001062	HRIFA023434a

Table 18

The representative sequences of the most homologous sequenses in the SwissProt with the keyword(s) "extracellular matrix", and the selected clones.	
name of clone	name of representative sequence
HEMBA1000006	HRIFA027327a
HEMBA1000275	HRIFA000264a
HEMBA1000835	HRIFA000776a
HEMBA1000907	HRIFA000845a
HEMBA1002164	HRIFA001972a
HEMBA1003101	HRIFA002787a
HEMBA1003230	HRIFA002891a
MAMMA1000403	HRIFA026465a
MAMMA1001615	HRIFA022865a
MAMMA1001893	HRIFA027485a
MAMMA1002128	HRIFA027644a
NT2RM4000284	HRIFA032506a
NT2RM4000295	HRIFA032511a
NT2RM4000587	HRIFA032696a
NT2RP2000616	HRIFA006572a
NT2RP2000694	HRIFA006633a
NT2RP2001562	HRIFA010799a
NT2RP2001948	HRIFA007565a
NT2RP2002409	HRIFA007909a
NT2RP2004447	HRIFA009339a
NT2RP2004847	HRIFA005944a
NT2RP2006004	HRIFA002766a
NT2RP3000059	HRIFA022203a
NT2RP3000616	HRIFA022875a

Table 18 (continued)

The representative sequences of the most homologous sequenses in the SwissProt with the keyword(s) "extracellular matrix", and the selected clones.	
name of clone	name of representative sequence
NT2RP3000871	HRIFA023048a
NT2RP3000921	HRIFA023069a
NT2RP3002015	HRIFA015995a
NT2RP3002448	HRIFA024218a
NT2RP3002983	HRIFA024473a
NT2RP3003729	HRIFA025488a
NT2RP3004067	HRIFA027327a
OVARC1001049	HRIFA022702a
OVARC1001222	HRIFA022714a
OVARC1002058	HRIFA022737a
PLACE1001114	HRIFA012427a
PLACE1002329	HRIFA013235a
PLACE1004816	HRIFA014819a
PLACE1005383	HRIFA015219a
PLACE1005569	HRIFA015351a
PLACE1006073	HRIFA003402a
PLACE1006277	HRIFA015802a
PLACE1008984	HRIFA017456a
THYR01001102	HRIFA008174a
THYRO1001471	HRIFA030381a
THYRO1001478	HRIFA030385a
Y79AA1000888	HRIFA028440a

Table 19

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "transmembrane", and the selected clones (except overlapped with Table 16, 17, and 18)	
name of clone	name of representative sequence
BNGH41000020	HRIFA030662a
HEMBA1000121	HRIFA000116a
HEMBA1000349	HRIFA000327a
HEMBA1000477	HRIFA000446a
HEMBA1000940	HRIFA002384a
HEMBA1002163	HRIFA001971a
HEMBA1002421	HRIFA005392a
HEMBA1002767	HRIFA002503a
HEMBA1003945	HRIFA009220a
HEMBA1004250	HRIFA003504a
HEMBA1004391	HRIFA020693a
HEMBA1004444	HRIFA029285a
HEMBA1004454	HRIFA003592a
HEMBA1004505	HRIFA003635a
HEMBA1004797	HRIFA020883a
HEMBA1004982	HRIFA003892a
HEMBA1005489	HRIFA024543a
HEMBA1005698	HRIFA020453a
HEMBA1005945	HRIFA020349a

Table 19 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "transmembrane", and the selected clones (except overlapped with Table 16, 17, and 18)	
name of clone	name of representative sequence
HEMBA1006299	HRIFA025771a
HEMBA1006430	HRIFA021213a
HEMBA1006482	HRIFA022328a
HEMBA1007241	HRIFA022423a
HEMBB1000679	HRIFA029802a
HEMBB1001200	HRIFA030839a
HEMBB1001573	HRIFA031091a
HEMBB1002427	HRIFA005760a
MAMMA1000204	HRIFA025966a
MAMMA1000473	HRIFA018870a
MAMMA1000196	HRIFA026242a
MAMMA1000788	HRIFA018287a
MAMMA1000814	HRIFA026618a
MAMMA1001237	HRIFA026860a
MAMMA1001418	HRIFA027045a
MAMMA1002091	HRIFA027622a
MAMMA1002095	HRIFA027625a
MAMMA1002586	HRIFA027012a
NT2RM1000580	HRIFA004523a
NT2RM1000855	HRIFA004696a
NT2RM1000858	HRIFA004714a
NT2RM1000899	HRIFA004745a
NT2RM2000565	HRIFA022139a
NT2RM2000582	HRIFA021787a
NT2RM2001126	HRIFA024088a
NT2RM4000198	HRIFA032453a
NT2RM4000417	HRIFA032587a
NT2RM4000444	HRIFA032605a
NT2RM4000593	HRIFA023489a
NT2RM4000761	HRIFA023923a
NT2RM4000965	HRIFA030103a
NT2RM4001735	HRIFA002063a
NT2RP1000181	HRIFA005184a
NT2RP1000261	HRIFA005231a
NT2RP1000300	HRIFA005255a
NT2RP1000325	HRIFA005271a
NT2RP1000551	HRIFA005420a
NT2RP1000981	HRIFA005702a
NT2RP2000533	HRIFA006510a
NT2RP2000649	HRIFA006596a
NT2RP2000818	HRIFA006730a
NT2RP2001200	HRIFA007013a
NT2RP2001495	HRIFA007228a
NT2RP2001514	HRIFA007243a
NT2RP2001956	HRIFA007571a
NT2RP2002063	HRIFA007659a
NT2RP2002232	HRIFA009783a

Table 19 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "transmembrane", and the selected clones (except overlapped with Table 16, 17, and 18)	
name of clone	name of representative sequence
NT2RP2002527	HRIFA023767a
NT2RP2002942	HRIFA008284a
NT2RP2002976	HRIFA008314a
NT2RP2003210	HRIFA008483a
NT2RP2003390	HRIFA008611a
NT2RP2003469	HRIFA008661a
NT2RP2003655	HRIFA008784a
NT2RP2003664	HRIFA008790a
NT2RP2004205	HRIFA009171a
NT2RP2004794	HRIFA009578a
NT2RP2005425	HRIFA010005a
NT2RP2005597	HRIFA010130a
NT2RP2005632	HRIFA010152a
NT2RP2005994	HRIFA010394a
NT2RP2006269	HRIFA025913a
NT2RP2006512	HRIFA024937a
NT2RP3000125	HRIFA022234a
NT2RP3000171	HRIFA007722a
NT2RP3000676	HRIFA026576a
NT2RF3000907	HRIFA025046a
NT2RP3001061	HRIFA023154a
NT2RP3001170	HRIFA010078a
NT2RP3001195	HRIFA023227a
NT2RP3001240	HRIFA023257a
NT2RP3001322	HRIFA023304a
NT2RP3001388	HRIFA006926a
NT2RP3001560	HRIFA030599a
NT2RP3001738	HRIFA025766a
NT2RP3002160	HRIFA005760a
NT2RP3002324	HRIFA024884a
NT2RP3002342	HRIFA006586a
NT2RP3002571	HRIFA024255a
NT2RP3002900	HRIFA024423a
NT2RP3002958	HRIFA017670a
NT2RP3003532	HRIFA013477a
NT2RP3003939	HRIFA025636a
NT2RP3004130	HRIFA025703a
NT2RP3004133	HRIFA025706a
NT2RP3004294	HRIFA025771a
NT2RP3004406	HRIFA025800a
NT2RP3004481	HRIFA026089a
NT2RP3004625	HRIFA026564a
NT2RP3004647	HRIFA026576a
NT2RP4001009	HRIFA022227a
NT2RP4001879	HRIFA017818a
OVARC1000003	HRIFA010790a
OVARC1000105	HRIFA007493a

Table 19 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "transmembrane", and the selected clones (except overlapped with Table 16, 17, and 18)	
name of clone	name of representative sequence
OVARC1000137	HRIFA010891a
OVARC1000307	HRIFA002919a
OVARC1000331	HRIFA004162a
OVARC1000553	HRIFA011197a
OVARC1000873	HRIFA032478a
OVARC1001163	HRIFA032079a
OVARC1001260	HRIFA019867a
OVARC1001336	HRIFA019867a
OVARC1001607	HRIFA022729a
PLACE1000740	HRIFA012151a
PLACE1001123	HRIFA012436a
PLACE1001231	HRIFA012515a
PLACE1001836	HRIFA012914a
PLACE1001949	HRIFA012990a
PLACE1002095	HRIFA013103a
PLACE1002905	HRIFA013586a
PLACE1002911	HRIFA013589a
PLACE1003163	HRIFA013744a
PLACE1003644	HRIFA014056a
PLACE1003737	HRIFA014111a
PLACE1004279	HRIFA014465a
PLACE1004450	HRIFA014568a
PLACE1004482	HRIFA014590a
PLACE1004630	HRIFA014688a
PLACE1005544	HRIFA009852a
PLACE1005745	HRIFA017855a
PLACE1005927	HRIFA015568a
PLACE1006290	HRIFA015811a
PLACE1007096	HRIFA012167a
PLACE1007845	HRIFA016758a
PLACE1007881	HRIFA016240a
PLACE1008359	HRIFA015547a
PLACE1008716	HRIFA017295a
PLACE1008985	HRIFA017457a
PLACE1009600	HRIFA017836a
PLACE1010011	HRIFA018092a
PLACE1010078	HRIFA018131a
PLACE1010251	HRIFA018238a
PLACE1010445	HRIFA010736a
PLACE1010827	HRIFA018580a
PLACE1011045	HRIFA014500a
PLACE1011181	HRIFA018794a
PLACE1011236	HRIFA018827a
PLACE1011516	HRIFA018993a
PLACE3000181	HRIFA004112a
SKNMC1000082	HRIFA030147a
THYRO1000196	HRIFA029050a

Table 19 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "transmembrane", and the selected clones (except overlapped with Table 16, 17, and 18)	
name of clone	name of representative sequence
THYRO1000400	HRIFA000564a
THYRO1000584	HRIFA029209a
THYRO1000678	HRIFA029256a
THYRO1000776	HRIFA029317a
THYRO1000795	HRIFA029327a
THYRO1000866	HRIFA027714a
THYRO1001113	HRIFA029460a
THYRO1001128	HRIFA029467a
THYRO1001242	HRIFA032360a
THYRO1001266	HRIFA030264a
THYRO1001456	HRIFA030370a
THYRO1001529	HRIFA030411a
THYRO1001702	HRIFA030511a
Y79AA1000127	HRIFA026121a
Y79AA1000270	HRIFA005644a
Y79AA1001426	HRIFA028651a
Y79AA1001787	HRIFA028790a
Y79AA1001799	HRIFA032070a
Y79AA1002213	HRIFA032224a

Table 20

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "signal", and the selected clones (except overlapped with Table 16, 17, 18 and 19)	
name of clone	name of representative sequence
BNGH41000087	HRIFA029508a
HEMBA1000128	HRIFA000123a
HEMBA1000443	HRIFA000415a
HEMBA1000590	HRIFA000553a
HEMBA1000634	HRIFA004780a
HEMBA1000745	HRIFA000695a
HEMBA1001221	HRIFA001132a
HEMBA1001228	HRIFA001138a
HEMBA1001390	HRIFA000071a
HEMBA1002131	HRIFA001942a
HEMBA1002167	HRIFA001975a
HEMBA1002178	HRIFA001984a
HEMBA1002524	HRIFA002284a
HEMBA1002992	HRIFA002694a
HEMBA1003072	HRIFA002762a
HEMBA1003315	HRIFA000016a
HEMBA1003487	HRIFA003055a
HEMBA1003530	HRIFA003093a
HEMBA1005145	HRIFA003946a
HEMBA1005337	HRIFA019651a
HEMBA1005449	HRIFA020707a
HEMBA1005522	HRIFA021398a

Table 20 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "signal", and the selected clones (except overlapped with Table 16, 17, 18 and 19)	
name of clone	name of representative sequence
HEMBA1006335	HRIFA012069a
HEMBA1006572	HRIFA021543a
HEMBA1006707	HRIFA021499a
HEMBA1006749	HRIFA021637a
HEMBA1006902	HRIFA021754a
HEMBA1007013	HRIFA021906a
HEMBA1007057	HRIFA022985a
HEMBB1000447	HRIFA001558a
HEMBB1000567	HRIFA029730a
HEMBB1000881	HRIFA029932a
HEMBB1001026	HRIFA030025a
HEMBB1001048	HRIFA030045a
HEMBB1001847	HRIFA031249a
MAMMA1000106	HRIFA024482a
MAMMA1000226	HRIFA025978a
MAMMA1000591	HRIFA026303a
MAMMA1001043	HRIFA026764a
MAMMA1001957	HRIFA027536a
MAMMA1002080	HRIFA016963a
MAMMA1002234	HRIFA027722a
MAMMA1002633	HRIFA030461a
MAMMA1003126	HRIFA029263a
NT2RM1000462	HRIFA004426a
NT2RM1000542	HRIFA004490a
NT2RM2000410	HRIFA022055a
NT2RM2000423	HRIFA022065a
NT2RM2000622	HRIFA022156a
NT2RM2000773	HRIFA023894a
NT2RM2001626	HRIFA028911a
NT2RM2001818	HRIFA031935a
NT2RM4000648	HRIFA032730a
NT2RM4001843	HRIFA024718a
NT2RP1000050	HRIFA005102a
NT2RP1001004	HRIFA005720a
NT2RP2000394	HRIFA003640a
NT2RP2000514	HRIFA006494a
NT2RP2001480	HRIFA007219a
NT2RP2001755	HRIFA007424a
NT2RP2001878	HRIFA007512a
NT2RP2002188	HRIFA007745a
NT2RP2002564	HRIFA007244a
NT2RP2002824	HRIFA008200a
NT2RP2003042	HRIFA008362a
NT2RP2003593	HRIFA008252a
NT2RP2003931	HRIFA008976a
NT2RP2004606	HRIFA009451a
NT2RP2004648	HRIFA009482a

Table 20 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "signal", and the selected clones (except overlapped with Table 16, 17, 18 and 19)	
name of clone	name of representative sequence
NT2RP2005163	HRIFA009825a
NT2RP2005247	HRIFA009881a
NT2RP2005378	HRIFA004919a
NT2RP2005541	HRIFA010090a
NT2RP2005883	HRIFA010319a
NT2RP2006042	HRIFA010425a
NT2RP3000063	HRIFA022528a
NT2RP3000436	HRIFA022776a
NT2RP3000444	HRIFA022782a
NT2RP3000481	HRIFA028614a
NT2RP3000721	HRIFA009825a
NT2RP3001012	HRIFA023129a
NT2RP3001159	HRIFA023212a
NT2RP3001592	HRIFA023464a
NT2RP3001754	HRIFA007728a
NT2RP3002311	HRIFA024718a
NT2RP3002738	HRIFA020748a
NT2RP3002790	HRIFA026519a
NT2RP3002887	HRIFA029278a
NT2RP3003354	HRIFA008212a
NT2RP3003448	HRIFA025479a
NT2RP3003473	HRIFA001413a
NT2RP3003614	HRIFA032642a
NT2RP3004075	HRIFA010301a
NT2RP3004090	HRIFA027329a
NT2RP3004202	HRIFA025327a
NT2RP3004309	HRIFA025778a
NT2RP3004345	HRIFA025353a
NT2RP3004557	HRIFA025907a
NT2RP4001467	HRIFA013276a
OVARC1000313	HRIFA011016a
OVARC1000410	HRIFA022691a
OVARC1000439	HRIFA011105a
OVARC1001086	HRIFA011580a
OVARC1001569	HRIFA022728a
OVARC1001570	HRIFA019412a
PLACE1001407	HRIFA012069a
PLACE1001464	HRIFA013276a
PLACE1001516	HRIFA012702a
PLACE1001795	HRIFA012885a
PLACE1001918	HRIFA012969a
PLACE1002080	HRIFA0130921a
PLACE1002153	HRIFA013135a
PLACE1002355	HRIFA013254a
PLACE1002374	HRIFA013265a
PLACE1002726	HRIFA018688a
PLACE1003428	HRIFA013911a

Table 20 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "signal", and the selected clones (except overlapped with Table 16, 17, 18 and 19)	
name of clone	name of representative sequence
PLACE1003460	HRIFA013932a
PLACE1003772	HRIFA014133a
PLACE1004078	HRIFA014336a
PLACE1004520	HRIFA014621a
PLACE1004648	HRIFA014702a
PLACE1004887	HRIFA014868a
PLACE1005426	HRIFA015246a
PLACE1006071	HRIFA016639a
PLACE1006443	HRIFA015902a
PLACE1006716	HRIFA016070a
PLACE1006959	HRIFA016214a
PLACE1007077	HRIFA016639a
PLACE1007081	HRIFA016290a
PLACE1007702	HRIFA016669a
PLACE1008657	HRIFA017257a
PLACE1008744	HRIFA017312a
PLACE1009546	HRIFA017801a
PLACE1011116	HRIFA018754a
PLACE1011708	HRIFA019105a
PLACE2000118	HRIFA024994a
PLACE3000213	HRIFA015486a
PLACE4000354	HRIFA015486a
THYRO1000061	HRIFA013279a
THYRO1000846	HRIFA029349a
THYRO1001063	HRIFA029434a
THYRO1001608	HRIFA050456a
THYRO1001803	HRIFA030566a
Y79AA1000876	HRIFA030629a
Y79AA1001090	HRIFA028511a
Y79AA1001272	HRIFA028576a
Y79AA1001727	HRIFA006642a
Y79AA1001803	HRIFA032073a
Y79AA1002376	HRIFA032820a

Table 21

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "glycoprotein", and the selected clones	
name of clone	name of representative sequence
BNGH41000087	HRIFA029508a
BNGH41000091	HRIFA029511a
HEMBA1000275	HRIFA000264a
HEMBA1000349	HRIFA000327a
HEMBA1000590	HRIFA000553a
HEMBA1000634	HRIFA004780a
HEMBA1000835	HRIFA000776a
HEMBA1000907	HRIFA000845a

Table 21 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "glycoprotein", and the selected clones	
name of clone	name of representative sequence
HEMBA1001221	HRIFA001132a
HEMBA1001228	HRIFA001138a
HEMBA1001621	HRIFA001489a
HEMBA1002131	HRIFA001942a
HEMBA1002164	HRIFA001972a
HEMBA1002167	HRIFA001975a
HEMBA1002178	HRIFA001984a
HEMBA1002316	HRIFA002102a
HEMBA1002421	HRIFA005392a
HEMBA1002767	HRIFA002503a
HEMBA1003047	HRIFA002743a
HEMBA1003101	HRIFA002787a
HEMBA1003230	HRIFA002891a
HEMBA1003392	HRIFA002980a
HEMBA1004250	HRIFA003504a
HEMBA1004391	HRIFA020693a
HEMBA1004444	HRIFA029285a
HEMBA1004454	HRIFA003592a
HEMBA1004505	HRIFA003635a
HEMBA1005449	HRIFA020707a
HEMBA1005489	HRIFA024543a
HEMBA1005522	HRIFA021398a
HEMBA1005545	HRIFA020272a
HEMBA1006335	HRIFA012069a
HEMBA1006572	HRIFA021543a
HEMBA1006707	HRIFA021499a
HEMBA1006724	HRIFA021620a
HEMBA1006749	HRIFA021637a
HEMBA1006902	HRIFA021754a
HEMBA1007057	HRIFA022985a
HEMBA1007332	HRIFA022493a
HEMBB1000447	HRIFA001558a
HEMBB1000567	HRIFA029730a
HEMBB1000679	HRIFA029802a
HEMBB1000881	HRIFA029932a
HEMBB1001048	HRIFA030045a
HEMBB1002427	HRIFA005760a
MAMMA1000106	HRIFA024482a
MAMMA1000403	HRIFA026465a
MAMMA1000591	HRIFA026303a
MAMMA1000681	HRIFA026364a
MAMMA1000706	HRIFA026382a
MAMMA1001043	HRIFA026764a
MAMMA1001237	HRIFA026860a
MAMMA1001615	HRIFA022865a
MAMMA1001893	HRIFA027485a
MAMMA1001978	HRIFA027549a

Table 21 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "glycoprotein", and the selected clones	
name of clone	name of representative sequence
MAMMA1002070	HRIFA028371a
MAMMA1001091	HRIFA027622a
MAMMA1002128	HRIFA027644a
MAMMA1002586	HRIFA027012a
MAMMA1003126	HRIFA029263a
NT2RM1000462	HRIFA004426a
NT2RM1000542	HRIFA004490a
NT2RM1000580	HRIFA004523a
NT2RM2000423	HRIFA022065a
NT2RM2001626	HRIFA028911a
NT2RM2001792	HRIFA029002a
NT2RM2001818	HRIFA031935a
NT2RM2001939	HRIFA032009a
NT2RM2001941	HRIFA032011a
NT2RM4000198	HRIFA032453a
NT2RM4000284	HRIFA032506a
NT2RM4000417	HRIFA032587a
NT2RM4000587	HRIFA032696a
NT2RM4000648	HRIFA032730a
NT2RM4001843	HRIFA024718a
NT2RM4002352	HRIFA001337a
NT2RP1000002	HRIFA005072a
NT2RP1000050	HRIFA005102a
NT2RP1000613	HRIFA005462a
NT2RP1000981	HRIFA005702a
NT2RP1001004	HRIFA005720a
NT2RP2000394	HRIFA003640a
NT2RP2000514	HRIFA006494a
NT2RP2000616	HRIFA006572a
NT2RP2001480	HRIFA007219a
NT2RP2001562	HRIFA010799a
NT2RP2001755	HRIFA007424a
NT2RP2001878	HRIFA007512a
NT2RP2002188	HRIFA007745a
NT2RP2002304	HRIFA007829a
NT2RP2002409	HRIFA007909a
NT2RP2002510	HRIFA007985a
NT2RP2002533	HRIFA008000a
NT2RP2002564	HRIFA007244a
NT2RP2002942	HRIFA008284a
NT2RP2003042	HRIFA008362a
NT2RP2003469	HRIFA008661a
NT2RP2003931	HRIFA008976a
NT2RP2004205	HRIFA009171a
NT2RP2004447	HRIFA009339a
NT2RP2004606	HRIFA009451a
NT2RP2004648	HRIFA009482a

Table 21 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "glycoprotein", and the selected clones	
name of clone	name of representative sequence
NT2RP2004847	HRIFA005944a
NT2RP2005181	HRIFA005409a
NT2RP2005247	HRIFA009881a
NT2RP2005541	HRIFA010090a
NT2RP2005597	HRIFA010130a
NT2RP2005632	HRIFA010152a
NT2RP2005883	HRIFA010319a
NT2RP2006004	HRIFA002766a
NT2RP2006042	HRIFA010425a
NT2RP2006269	HRIFA025913a
NT2RP3000059	HRIFA022203a
NT2RP3000063	HRIFA022528a
NT2RP3000125	HRIFA022234a
NT2RP3000304	HRIFA022616a
NT2RP3000481	HRIFA028614a
NT2RP3000616	HRIFA022875a
NT2RP3000871	HRIFA023048a
NT2RP3000921	HRIFA023069a
NT2RP3001012	HRIFA023129a
NT2RP3001061	HRIFA023154a
NT2RP3001159	HRIFA023212a
NT2RP3001542	HRIFA028501a
NT2RP3001560	HRIFA030599a
NT2RP3001754	HRIFA007728a
NT2RP3002015	HRIFA015995a
NT2RP3002160	HRIFA005760a
NT2RP3002311	HRIFA024718a
NT2RP3002448	HRIFA024218a
NT2RP3002738	HRIFA020748a
NT2RP3002836	HRIFA024392a
NT2RP3002958	HRIFA017670a
NT2RP3002983	HRIFA024473a
NT2RP3003000	HRIFA024767a
NT2RP3003076	HRIFA024978a
NT2RP3003354	HRIFA008212a
NT2RP3003532	HRIFA013477a
NT2RP3003729	HRIFA025488a
NT2RP3004130	HRIFA025703a
NT2RP3004133	HRIFA025706a
NT2RP3004309	HRIFA025778a
NT2RP3004481	HRIFA026089a
NT2RP3004552	HRIFA025904a
NT2RP3004625	HRIFA026564a
NT2RP3004640	HRIFA030250a
NT2RP4000108	HRIFA001341a
NT2RP4001467	HRIFA013276a
NT2RP4001877	HRIFA032433a

Table 21 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "glycoprotein", and the selected clones	
name of clone	name of representative sequence
NT2RP4002750	HRIFA028157a
OVARC1000003	HRIFA010790a
OVARC1000090	HRIFA010859a
OVARC1000313	HRIFA011016a
OVARC1000467	HRIFA011128a
OVARC1000553	HRIFA011197a
OVARC1000873	HRIFA032478a
OVARC1000956	HRIFA011484a
OVARC1001049	HRIFA022702a
OVARC1001086	HRIFA011580a
OVARC1001260	HRIFA019867a
OVARC1001336	HRIFA019867a
OVARC1001569	HRIFA022728a
OVARC1001570	HRIFA019412a
OVARC1001607	HRIFA022729a
OVARC1001991	HRIFA019498a
OVARC1002058	HRIFA022737a
PLACE1000740	HRIFA012151a
PLACE1001016	HRIFA012354a
PLACE1001114	HRIFA012427a
PLACE1001123	HRIFA012436a
PLACE1001231	HRIFA012515a
PLACE1001407	HRIFA012069a
PLACE1001464	HRIFA013276a
PLACE1001516	HRIFA012702a
PLACE1001564	HRIFA012737a
PLACE1001655	HRIFA012795a
PLACE1001836	HRIFA012914a
PLACE1002095	HRIFA013103a
PLACE1002329	HRIFA013235a
PLACE1002355	HRIFA013254a
PLACE1002374	HRIFA013265a
PLACE1002905	HRIFA013586a
PLACE1002911	HRIFA013589a
PLACE1003163	HRIFA013744a
PLACE1003428	HRIFA013911a
PLACE1003438	HRIFA013919a
PLACE1003573	HRIFA014006a
PLACE1003737	HRIFA014111a
PLACE1003852	HRIFA014185a
PLACE1004441	HRIFA014561a
PLACE1004450	HRIFA014568a
PLACE1004520	HRIFA014621a
PLACE1004630	HRIFA014688a
PLACE1004816	HRIFA014819a
PLACE1005003	HRIFA014951a
PLACE1005383	HRIFA015219a

Table 21 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "glycoprotein", and the selected clones	
name of clone	name of representative sequence
PLACE1005426	HRIFA015246a
PLACE1005539	HRIFA029425a
PLACE1005544	HRIFA009852a
PLACE1005569	HRIFA015351a
PLACE1006071	HRIFA016639a
PLACE1006073	HRIFA003402a
PLACE1006277	HRIFA015802a
PLACE1006290	HRIFA015811a
PLACE1006443	HRIFA015902a
PLACE1006716	HRIFA016070a
PLACE1007077	HRIFA016639a
PLACE1007081	HRIFA016290a
PLACE1007845	HRIFA016758a
PLACE1008469	HRIFA017146a
PLACE1008716	HRIFA017295a
PLACE1008744	HRIFA017312a
PLACE1008984	HRIFA017456a
PLACE1008985	HRIFA017457a
PLACE1009527	HRIFA017791a
PLACE1010251	HRIFA018238a
PLACE1010784	HRIFA031126a
PLACE1010968	HRIFA018666a
PLACE1011116	HRIFA018754a
PLACE1011708	HRIFA019105a
PLACE2000118	HRIFA024994a
PLACE3000181	HRIFA004112a
PLACE3000213	HRIFA015486a
PLACE4000354	HRIFA015486a
SKNMC1000014	HRIFA030106a
THYRO1000196	HRIFA029050a
THYRO1000584	HRIFA029209a
THYRO1000956	HRIFA029393a
THYRO1001102	HRIFA008174a
THYRO1001128	HRIFA029467a
THYRO1001266	HRIFA030264a
THYRO1001803	HRIFA030566a
Y79AA1000127	HRIFA026121a
Y79AA1000207	HRIFA027867a
Y79AA1000270	HRIFA005644a
Y79AA1000426	HRIFA027940a
Y79AA1000888	HRIFA028440a
Y79AA1001062	HRIFA023434a
Y79AA1001272	HRIFA028576a
Y79AA1001426	HRIFA028651a
Y79AA1001523	HRIFA030642a
Y79AA1001727	HRIFA006642a
Y79AA1001863	HRIFA032097a

Table 22

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "serine/threonine-protein kinase", "tyrosine-protein kinase", or "calmodulin-binding", and the selected clones	
name of clone	name of representative sequence
HEMBA1001878	HRIFA001712a
HEMBA1002195	HRIFA017703a
HEMBA1002227	HRIFA019136a
HEMBA1002551	HRIFA002309a
HEMBA1005084	HRIFA020184a
HEMBA1005913	HRIFA029866a
HEMBA1005929	HRIFA020335a
HEMBB1000668	HRIFA029792a
MAMMA1000881	HRIFA026659a
MAMMA1001150	HRIFA026813a
MAMMA1002142	HRIFA027656a
NT2RM2000589	HRIFA021794a
NT2RM2001902	HRIFA031986a
NT2PP1001020	HRIFA005728a
NT2RP1001031	HRIFA005732a
NT2RP2001469	HRIFA028061a
NT2RP2001529	HRIFA007256a
NT2RP2001769	HRIFA007435a
NT2RP2003179	HRIFA008459a
NT2RP2003545	HRIFA008717a
NT2RP2004670	HRIFA028468a
NT2RP3000011	HRIFA022177a
NT2RP3000022	HRIFA022182a
NT2RP3000172	HRIFA022265a
NT2RP3000201	HRIFA022546a
NT2RP3000820	HRIFA018262a
NT2RP3003527	HRIFA025492a
NT2RP3003849	HRIFA025250a
NT2RP3003874	HRIFA025261a
NT2RP4000634	HRIFA029866a
NT2RP4000962	HRIFA027681a
OVARC1000255	HRIFA010975a
OVARC1000529	HRIFA011179a
OVARC1000916	HRIFA011449a
OVARC1001338	HRIFA019869a
PLACE1003135	HRIFA013726a
PLACE1005519	HRIFA015070a
PLACE1005736	HRIFA015453a
PLACE1008282	HRIFA016654a
PLACE1008297	HRIFA017031a
PLACE1010081	HRIFA018134a
PLACE1011364	HRIFA018904a
PLACE1011824	HRIFA019175a
THYRO1001205	HRIFA030237a
THYRO1001457	HRIFA030371a
THYRO1001593	HRIFA030448a

Table 22 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "serine/threonine-protein kinase", "tyrosine-protein kinase", or "calmodulin-binding", and the selected clones	
name of clone	name of representative sequence
THYRO1001700	HRIFA030509a
THYRO1001770	HRIFA030545a
Y79AA1000777	HRIFA028402a
Y79AA1000967	HRIFA028468a
Y79AA1002381	HRIFA032275a

Table 23

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "transcription regulation" and "activator", "transcription regulation" and "repressor", or "nuclear protein" and "repressor", and the selected clones	
name of clone	name of representative sequence
HEMBA1000462	HRIFA000432a
HEMBA1000671	HRIFA000631a
HEMBA1000875	HRIFA000814a
HEMBA1001184	HRIFA001099a
HEMBA1001296	HRIFA001200a
HEMBA1001886	HRIFA001720a
HEMBA1002048	HRIFA001866a
HEMBA1002985	HRIFA002689a
HEMBA1003120	HRIFA002805a
HEMBA1003497	HRIFA003063a
HEMBA1004007	HRIFA021040a
HEMBA1004067	HRIFA003340a
HEMBA1004085	HRIFA003357a
HEMBA1004785	HRIFA020862a
HEMBA1004952	HRIFA019532a
HEMBA1004971	HRIFA003883a
HEMBA1005230	HRIFA004006a
HEMBA1005246	HRIFA019490a
HEMBA1005267	HRIFA004034a
HEMBA1006276	HRIFA021224a
HEMBA1006517	HRIFA021445a
HEMBA1006544	HRIFA021494a
HEMBA1006770	HRIFA021651a
HEMBA1006912	HRIFA022335a
HEMBA1007063	HRIFA022348a
HEMBA1007226	HRIFA022411a
HEMBB1000106	HRIFA028262a
HEMBB1000309	HRIFA029602a
HEMBB1000407	HRIFA029649a
HEMBB1000542	HRIFA029715a
HEMBB1001959	HRIFA031336a
HEMBB1002039	HRIFA031395a
HEMBB1002041	HRIFA031397a
HEMBB1002051	HRIFA026351a
HEMBB1002120	HRIFA031438a

Table 23 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "transcription regulation" and "activator", "transcription regulation" and "repressor", or "nuclear protein" and "repressor", and the selected clones	
name of clone	name of representative sequence
HEMBB1002302	HRIFA009136a
HEMBB1002661	HRIFA031869a
MAMMA1000528	HRIFA026265a
MAMMA1000614	HRIFA026316a
MAMMA1000810	HRIFA026615a
MAMMA1001094	HRIFA026789a
MAMMA1001532	HRIFA027125a
MAMMA1001609	HRIFA027173a
NT2RM1000407	HRIFA004401a
NT2RM1000789	HRIFA004663a
NT2RM2001558	HRIFA028804a
NT2RM2001738	HRIFA028867a
NT2RM2001767	HRIFA028983a
NT2RM4000100	HRIFA032389a
NT2RP1000239	HRIFA005214a
NT2RP1000271	HRIFA005240a
NT2RP1000465	HRIFA005369a
NT2RP1000468	HRIFA005372a
NT2RP1000679	HRIFA005500a
NT2RP1000740	HRIFA005540a
NT2RP2000092	HRIFA006183a
NT2RP2000178	HRIFA006250a
NT2RP2000240	HRIFA006298a
NT2RP2000610	HRIFA006566a
NT2RP2000712	HRIFA006649a
NT2RP2000739	HRIFA006667a
NT2RP2001223	HRIFA007032a
NT2RP2001276	HRIFA007068a
NT2RP2001388	HRIFA007152a
NT2RP2001538	HRIFA007262a
NT2RP2001662	HRIFA007352a
NT2RP2001817	HRIFA007463a
NT2RP2001921	HRIFA007547a
NT2RP2003138	HRIFA008426a
NT2RP2003302	HRIFA008547a
NT2RP2003940	HRIFA008981a
NT2RP2003950	HRIFA008989a
NT2RP2004069	HRIFA009071a
NT2RP2004108	HRIFA009101a
NT2RP2005069	HRIFA009762a
NT2RP2005391	HRIFA009983a
NT2RP2005535	HRIFA010085a
NT2RP2005666	HRIFA010176a
NT2RP2005774	HRIFA015063a
NT2RP2006092	HRIFA010460a
NT2RP2006134	HRIFA010490a

Table 23 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "transcription regulation" and "activator", "transcription regulation" and "repressor", or "nuclear protein" and "repressor", and the selected clones	
name of clone	name of representative sequence
NT2RP3000148	HRIFA022249a
NT2RP3000232	HRIFA022564a
NT2RP3000378	HRIFA022671a
NT2RP3000427	HRIFA025033a
NT2RP3000652	HRIFA022895a
NT2RP3000677	HRIFA023007a
NT2RP3001271	HRIFA023634a
NT2RP3001650	HRIFA026923a
NT2RP3001976	HRIFA026496a
NT2RP3002286	HRIFA024185a
NT2RP3002353	HRIFA024893a
NT2RP3002664	HRIFA024305a
NT2RP3004025	HRIFA025290a
NT2RP3004119	HRIFA025695a
OVARC1000995	HRIFA011512a
OVARC1001132	HRIFA022707a
OVARC1001596	HRIFA019437a
OVARC1001725	HRIFA019958a
OVARC1001952	HRIFA019466a
OVARC1002178	HRIFA021007a
PLACE1000258	HRIFA011820a
PLACE1000442	HRIFA011947a
PLACE1000907	HRIFA012278a
PLACE1003529	HRIFA013980a
PLACE1003598	HRIFA014024a
PLACE1004166	HRIFA014396a
PLACE1004168	HRIFA014397a
PLACE1004519	HRIFA014620a
PLACE1005239	HRIFA015122a
PLACE1005682	HRIFA015423a
PLACE1006208	HRIFA015756a
PLACE1006515	HRIFA015947a
PLACE1007028	HRIFA016255a
PLACE1007591	HRIFA016599a
PLACE1008549	HRIFA017190a
PLACE1009735	HRIFA017921a
PLACE1011407	HRIFA018931a
PLACE1011978	HRIFA019262a
THYRO1000580	HRIFA029208a
THYRO1000964	HRIFA029398a
THYRO1001641	HRIFA030472a
Y79AA1000030	HRIFA025936a
179AA1000750	HRIFA028187a
Y79AA1001212	HRIFA005296a
Y79AA1002058	HRIFA032161a
Y79AA1002121	HRIFA032186a

Table 23 (continued)

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "transcription regulation" and "activator", "transcription regulation" and "repressor", or "nuclear protein" and "repressor", and the selected clones	
name of clone	name of representative sequence
Y79AA1002129	HRIFA011926a
Y79AA1002334	HRIFA032257a
Y79AA1002378	HRIFA032274a

Table 24

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "disease mutation", or "syndrome", and the selected clones	
name of clone	name of representative sequence
HEMBA1000732	HRIFA000683a
HEMBA1000835	HRIFA000776a
HEMBA1004391	HRIFA020693a
MAMMA1001623	HRIFA027179c
NT2RM2000497	HRIFA021781a
NT2RM2000632	HRIFA022166a
NT2RP1000579	HRIFA005438a
NT2RP2001903	HRIFA007532a
NT2RP2005878	HRIFA008186a
NT2RP3002411	HRIFA005781a
NT2RP3002737	HRIFA024132a
NT2RP4002187	HRIFA030342a
PLACE1000033	HRIFA011659a
PLACE1001500	HRIFA012692a
PLACE1005815	HRIFA015506a
PLACE1008657	HRIFA017257a
PLACE1010713	HRIFA024504a

Table 25

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0.5 or higher.		
name of clone	name of sequence	maximal ATGpr1 score
BNGH41000020	F-BNGH41000020	0.94
BNGH41000087	F-BNGH41000087	0.57
BNGH41000091	F-BNGH41000091	0.81
HEMBA1000121	F-HEMBA1000121	0.94
HEMBA1000128	F-HEMBA1000128	0.81
HEMBA1000275	F-HEMBA1000275	0.83
HEMBA1000349	F-HEMBA1000349	0.52
HEMBA1000443	F-HEMBA1000443	0.56
HEMBA1000462	F-HEMBA1000462	0.75
HEMBA1000477	F-HEMBA1000477	0.55
HEMBA1000590	F-HEMBA1000590	0.75
HEMBA1000634	F-HEMBA1000634	0.94
HEMBA1000671	F-HEMBA1000671	0.65

Table 25 (continued)

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0.5 or higher.		
name of clone	name of sequence	maximal ATGpr1 score
HEMBA1000745	F-HEMBA1000745	0.78
HEMBA1000835	F-HEMBA1000835	0.64
HEMBA1000907	F-HEMBA1000907	0.94
HEMBA1000940	F-HEMBA1000940	0.86
HEMBA1001184	F-HEMBA1001184	0.54
HEMBA1001221	F-HEMBA1001221	0.89
HEMBA1001228	F-HEMBA1001228	0.94
HEMBA1001390	F-HEMBA1001390	0.90
HEMBA1001621	F-HEMBA1001621	0.94
HEMBA1001878	F-HEMBA1001878	0.92
HEMBA1002048	F-HEMBA1002048	0.71
HEMBA1002131	F-HEMBA1002131	0.94
HEMBA1002164	F-HEMBA1002164	0.74
HEMBA1002167	F-HEMBA1002167	0.94
HEMBA1002178	F-HEMBA1002178	0.91
HEMBA1002316	F-HEMBA1002316	0.73
HEMBA1002421	F-HEMBA1002421	0.90
HEMBA1002524	F-HEMBA1002524	0.80
HEMBA1002551	F-HEMBA1002551	0.60
HEMBA1002767	F-HEMBA1002767	0.94
HEMBA1002985	F-HEMBA1002985	0.90
HEMBA1002992	F-HEMBA1002992	0.76
HEMBA1003047	F-HEMBA1003047	0.70
HEMBA1003072	F-HEMBA1003072	0.94
HEMBA1003101	F-HEMBA1003101	0.94
HEMBA1003230	F-HEMBA1003230	0.77
HEMBA1003315	F-HEMBA1003315	0.76
HEMBA1003392	F-HEMBA1003392	0.94
HEMBA1003487	F-HEMBA1003487	0.90
HEMBA1003497	F-HEMBA1003497	0.61
HEMBA1003530	F-HEMBA1003530	0.94
HEMBA1003945	F-HEMBA1003945	0.94
HEMBA1004085	F-HEMBA1004085	0.59
HEMBA1004250	F-HEMBA1004250	0.83
HEMBA1004391	F-HEMBA1004391	0.94
HEMBA1004444	F-HEMBA1004444	0.94
HEMBA1004454	F-HEMBA1004454	0.50
HEMBA1004505	F-HEMBA1004505	0.94
HEMBA1004785	F-HEMBA1004785	0.89
HEMBA1004797	F-HEMBA1004797	0.66
HEMBA1004982	F-HEMBA1004982	0.55
HEMBA1005070	F-HEMBA1005070	0.94
HEMBA1005084	F-HEMBA1005084	0.89
HEMBA1005145	F-HEMBA1005145	0.85
HEMBA1005337	F-HEMBA1005337	0.62
HEMBA1005449	F-HEMBA1005449	0.91
HEMBA1005489	F-HEMBA1005489	0.70

Table 25 (continued)

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0.5 or higher.		
name of clone	name of sequence	maximal ATGpr1 score
HEMBA1005522	F-HEMBA1005522	0.73
HEMBA1005545	F-HEMBA1005545	0.94
HEMBA1005698	F-HEMBA1005698	0.68
HEMBA1005929	F-HEMBA1005929	0.72
HEMBA1005945	F-HEMBA1005945	0.80
HEMBA1006276	F-HEMBA1006276	0.50
HEMBA1006299	F-HEMBA1006299	0.94
HEMBA1006335	F-HEMBA1006335	0.94
HEMBA1006430	F-HEMBA1006430	0.93
HEMBA1006482	F-HEMBA1006482	0.59
HEMBA1006517	F-HEMBA1006517	0.68
HEMBA1006544	F-HEMBA1006544	0.94
HEMBA1006572	F-HEMBA1006572	0.62
HEMBA1006707	F-HEMBA1006707	0.94
HEMBA1006724	F-HEMBA1006724	0.80
HEMBA1006749	F-HEMBA1006749	0.94
HEMBA1006902	F-HEMBA1006902	0.94
HEMBA1006916	F-HEMBA1006916	0.80
HEMBA1007013	F-HEMBA1007013	0.82
HEMBA1007057	F-HEMBA1007057	0.94
HEMBA1007226	F-HEMBA1007226	0.50
HEMBA1007241	F-HEMBA1007241	0.94
HEMBB1000106	F-HEMBB1000106	0.94
HEMBB1000447	F-HEMBB1000447	0.73
HEMBB1000668	F-HEMBB1000668	0.50
HEMBB1000679	F-HEMBB1000679	0.91
HEMBB1000881	F-HEMBB1000881	0.77
HEMBB1001026	F-HEMBB1001026	0.94
HEMBB1001048	F-HEMBB1001048	0.88
HEMBB1001200	F-HEMBB1001200	0.81
HEMBB1001573	F-HEMBB1001573	0.80
HEMBB1001847	F-HEMBB1001847	0.81
HEMBB1001959	F-HEMBB1001959	0.94
HEMBB1002041	F-HEMBB1002041	0.79
HEMBB1002051	F-HEMBB1002051	0.60
HEMBB1002302	F-HEMBB1002302	0.89
HEMBB1002427	F-HEMBB1002427	0.94
HEMBB1002661	F-HEMBB1002661	0.94
MAMMA1000106	F-MAMMA1000106	0.78
MAMMA1000204	F-MAMMA1000204	0.94
MAMMA1000226	F-MAMMA1000226	0.94
MAMMA1000403	F-MAMMA1000403	0.59
MAMMA1000473	F-MAMMA1000473	0.86
MAMMA1000496	F-MAMMA1000496	0.70
MAMMA1000591	F-MAMMA1000591	0.77
MAMMA1000681	F-MAMMA1000681	0.94
MAMMA1000788	F-MAMMA1000788	0.83

Table 25 (continued)

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0.5 or higher.		
name of clone	name of sequence	maximal ATGpr1 score
MAMMA1000814	F-MAMMA1000814	0.94
MAMMA1000881	F-MAMMA1000881	0.51
MAMMA1001043	F-MAMMA1001043	0.81
MAMMA1001094	F-MAMMA1001094	0.80
MAMMA1001150	F-MAMMA1001150	0.91
MAMMA1001237	F-MAMMA1001237	0.52
MAMMA1001532	F-MAMMA1001532	0.52
MAMMA1001615	F-MAMMA1001615	0.94
MAMMA1001634	F-MAMMA1001634	0.94
MAMMA1001893	F-MAMMA1001893	0.90
MAMMA1001957	F-MAMMA1001957	0.94
MAMMA1002070	F-MAMMA1002070	0.82
MAMMA1002080	F-MAMMA1002080	0.72
MAMMA1002091	F-MAMMA1002091	0.70
MAMMA1002095	F-MAMMA1002095	0.85
MAMMA1002128	F-MAMMA1002128	0.79
MAMMA1002234	F-MAMMA1002234	0.94
MAMMA1002586	F-MAMMA1002586	0.67
MAMMA1002633	F-MAMMA1002633	0.94
MAMMA1003126	F-MAMMA1003126	0.94
NT2RM1000407	F-NT2RM1000407	0.94
NT2RM1000462	F-NT2RM1000462	0.94
NT2RM1000542	F-NT2RM1000542	0.94
NT2RM1000580	F-NT2RM1000580	0.94
NT2RM1000789	F-NT2RM1000789	0.82
NT2RM1000855	F-NT2RM1000855	0.94
NT2RM1000858	F-NT2RM1000858	0.50
NT2RM1000899	F-NT2RM1000899	0.78
NT2RM2000410	F-NT2RM2000410	0.82
NT2RM2000423	F-NT2RM2000423	0.66
NT2RM2000565	F-NT2RM2000565	0.56
NT2RM2000582	F-NT2RM2000582	0.78
NT2RM2000589	F-NT2RM2000589	0.86
NT2RM2000622	F-NT2RM2000622	0.94
NT2RM2000632	F-NT2RM2000632	0.73
NT2RM2000773	F-NT2RM2000773	0.64
NT2RM2001126	F-NT2RM2001126	0.87
NT2RM2001558	F-NT2RM2001558	0.94
NT2RM2001626	F-NT2RM2001626	0.68
NT2RM2001738	F-NT2RM2001738	0.94
NT2RM2001767	F-NT2RM2001767	0.82
NT2RM2001818	F-NT2RM2001818	0.70
NT2RM2001902	F-NT2RM2001902	0.69
NT2RM2001939	F-NT2RM2001939	0.55
NT2RM2001941	F-NT2RM2001941	0.94
NT2RM4000100	F-NT2RM4000100	0.74
NT2RM4000198	F-NT2RM4000198	0.85

Table 25 (continued)

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0.5 or higher.		
name of clone	name of sequence	maximal ATGpr1 score
NT2RM4000284	F-NT2RM4000284	0.89
NT2RM4000295	F-NT2RM4000295	0.74
NT2RM4000417	F-NT2RM4000417	0.82
NT2RM4000444	F-NT2RM4000444	0.94
NT2RM4000587	F-NT2RM4000587	0.94
NT2RM4000648	F-NT2RM4000648	0.88
NT2RM4000965	F-NT2RM4000965	0.60
NT2RM4001377	F-NT2RM4001377	0.82
NT2RM4001735	F-NT2RM4001735	0.94
NT2RM4002352	F-NT2RM4002352	0.83
NT2RP1000002	F-NT2RP1000002	0.76
NT2RP1000050	F-NT2RP1000050	0.54
NT2RP1000181	F-NT2RP1000181	0.73
NT2RP1000239	F-NT2RP1000239	0.94
NT2RP1000261	F-NT2RP1000261	0.57
NT2RP1000300	F-NT2RP1000300	0.94
NT2RP1000465	F-NT2RP1000465	0.94
NT2RP1000468	F-NT2RP1000468	0.94
NT2RP1000551	F-NT2RP1000551	0.94
NT2RP1000579	F-NT2RP1000579	0.94
NT2RP1000613	F-NT2RP1000613	0.90
NT2RP1000679	F-NT2RP1000679	0.68
NT2RP1000740	F-NT2RP1000740	0.80
NT2RP1000981	F-NT2RP1000981	0.94
NT2RP1001004	F-NT2RP1001004	0.74
NT2RP1001020	F-NT2RP1001020	0.70
NT2RP1001031	F-NT2RP1001031	0.59
NT2RP2000092	F-NT2RP2000092	0.88
NT2RP2000394	F-NT2RP2000394	0.94
NT2RP2000447	F-NT2RP2000447	0.50
NT2RP2000514	F-NT2RP2000514	0.82
NT2RP2000533	F-NT2RP2000533	0.94
NT2RP2000610	F-NT2RP2000610	0.94
NT2RP2000616	F-NT2RP2000616	0.80
NT2RP2000649	F-NT2RP2000649	0.53
NT2RP2000663	F-NT2RP2000663	0.88
NT2RP2000694	F-NT2RP2000694	0.74
NT2RP2000818	F-NT2RP2000818	0.54
NT2RP2000903	F-NT2RP2000903	0.59
NT2RP2001200	F-NT2RP2001200	0.88
NT2RP2001223	F-NT2RP2001223	0.92
NT2RP2001276	F-NT2RP2001276	0.59
NT2RP2001480	F-NT2RP2001480	0.85
NT2RP2001495	F-NT2RP2001495	0.78
NT2RP2001514	F-NT2RP2001514	0.78
NT2RP2001529	F-NT2RP2001529	0.94
NT2RP2001538	F-NT2RP2001538	0.89

Table 25 (continued)

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0.5 or higher.		
name of clone	name of sequence	maximal ATGpr1 score
NT2RP2001662	F-NT2RP2001662	0.94
NT2RP2001755	F-NT2RP2001755	0.94
NT2RP2001769	F-NT2RP2001769	0.66
NT2RP2001878	F-NT2RP2001878	0.68
NT2RP2001921	F-NT2RP2001921	0.61
NT2RP2001948	F-NT2RP2001948	0.89
NT2RP2001956	F-NT2RP2001956	0.74
NT2RP2002063	F-NT2RP2002063	0.94
NT2RP2002188	F-NT2RP2002188	0.78
NT2RP2002232	F-NT2RP2002232	0.90
NT2RP2002304	F-NT2RP2002304	0.94
NT2RP2002409	F-NT2RP2002409	0.94
NT2RP2002527	F-NT2RP2002527	0.58
NT2RP2002533	F-NT2RP2002533	0.87
NT2RP2002564	F-NT2RP2002564	0.94
NT2RP2002942	F-NT2RP2002942	0.66
NT2RP2002976	F-NT2RP2002976	0.94
NT2RP2003042	F-NT2RP2003042	0.93
NT2RP2003179	F-NT2RP2003179	0.94
NT2RP2003210	F-NT2RP2003210	0.61
NT2RP2003302	F-NT2RP2003302	0.79
NT2RP2003369	F-NT2RP2003369	0.93
NT2RP2003390	F-NT2RP2003390	0.79
NT2RP2003469	F-NT2RP2003469	0.90
NT2RP2003545	F-NT2RP2003545	0.55
NT2RP2003593	F-NT2RP2003593	0.94
NT2RP2003655	F-NT2RP2003655	0.83
NT2RP2003664	F-NT2RP2003664	0.89
NT2RP2004069	F-NT2RP2004069	0.76
NT2RP2004108	F-NT2RP2004108	0.91
NT2RP2004141	F-NT2RP2004141	0.53
NT2RP2004447	F-NT2RP2004447	0.93
NT2RP2004606	F-NT2RP2004606	0.94
NT2RP2004648	F-NT2RP2004648	0.94
NT2RP2004670	F-NT2RP2004670	0.94
NT2RP2004794	F-NT2RP2004794	0.65
NT2RP2004847	F-NT2RP2004847	0.94
NT2RP2005069	F-NT2RP2005069	0.89
NT2RP2005163	F-NT2RP2005163	0.79
NT2RP2005181	F-NT2RP2005181	0.87
NT2RP2005247	F-NT2RP2005247	0.77
NT2RP2005425	F-NT2RP2005425	0.77
NT2RP2005535	F-NT2RP2005535	0.51
NT2RP2005597	F-NT2RP2005597	0.74
NT2RP2005632	F-NT2RP2005632	0.87
NT2RP2005666	F-NT2RP2005666	0.77
NT2RP2005774	F-NT2RP2005774	0.87

Table 25 (continued)

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0.5 or higher.		
name of clone	name of sequence	maximal ATGpr1 score
NT2RP2005878	F-NT2RP2005878	0.70
NT2RP2005883	F-NT2RP2005883	0.94
NT2RP2005941	F-NT2RP2005941	0.81
NT2RP2005994	F-NT2RP2005994	0.62
NT2RP2006004	F-NT2RP2006004	0.61
NT2RP2006042	F-NT2RP2006042	0.69
NT2RP2006099	F-NT2RP2006099	0.65
NT2RP2006512	F-NT2RP2006512	0.94
NT2RP3000011	F-NT2RP3000011	0.93
NT2RP3000022	F-NT2RP3000022	0.55
NT2RP3000059	F-NT2RP3000059	0.74
NT2RP3000063	F-NT2RP3000063	0.78
NT2RP3000171	F-NT2RP3000171	0.72
NT2RP3000172	F-NT2RP3000172	0.93
NT2RP3000201	F-NT2RP3000201	0.50
NT2RP3000232	F-NT2RP3000232	0.61
NT2RP3000304	F-NT2RP3000304	0.94
NT2RP3000378	F-NT2RP3000378	0.56
NT2RP3000436	F-NT2RP3000436	0.65
NT2RP3000444	F-NT2RP3000444	0.94
NT2RP3000616	F-NT2RP3000616	0.77
NT2RP3000645	F-NT2RP3000645	0.91
NT2RP3000676	F-NT2RP3000676	0.94
NT2RP3000721	F-NT2RP3000721	0.82
NT2RP3000838	F-NT2RP3000838	0.94
NT2RP3000871	F-NT2RP3000871	0.94
NT2RP3000907	F-NT2RP3000907	0.59
NT2RP3000921	F-NT2RP3000921	0.64
NT2RP3001061	F-NT2RP3001061	0.72
NT2RP3001159	F-NT2RP3001159	0.94
NT2RP3001170	F-NT2RP3001170	0.70
NT2RP3001195	F-NT2RP3001195	0.94
NT2RP3001240	F-NT2RP3001240	0.83
NT2RP3001322	F-NT2RP3001322	0.62
NT2RP3001388	F-NT2RP3001388	0.94
NT2RP3001560	F-N12RP3001560	0.94
NT2RP3001592	F-NT2RP3001592	0.74
NT2RP3001650	F-NT2RP3001650	0.73
NT2RP3001738	F-N12RP3001738	0.94
NT2RP3002015	F-NT2RP3002015	0.93
NT2RP3002160	F-NT2RP3002160	0.65
NT2RP3002286	F-NT2RP3002286	0.82
NT2RP3002311	F-NT2RP3002311	0.94
NT2RP3002324	F-NT2RP3002324	0.92
NT2RP3002342	F-NT2RP3002342	0.94
NT2RP3002353	F-NT2RP3002353	0.76
NT2RP3002411	F-NT2RP3002411	0.74

Table 25 (continued)

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0.5 or higher.		
name of clone	name of sequence	maximal ATGpr1 score
NT2RP3002448	F-NT2RP3002448	0.87
NT2RP3002571	F-NT2RP3002571	0.61
NT2RP3002664	F-NT2RP3002664	0.82
NT2RP3002738	F-NT2RP3002738	0.81
NT2RP3002790	F-NT2RP3002790	0.94
NT2RP3002836	F-NT2RP3002836	0.72
NT2RP3002887	F-NT2RP3002887	0.94
NT2RP3002900	F-NT2RP3002900	0.88
NT2RP3002958	F-NT2RP3002958	0.91
NT2RP3002983	F-NT2RP3002983	0.92
NT2RP3003000	F-NT2RP3003000	0.80
NT2RP3003076	F-NT2RP3003076	0.65
NT2RP3003354	F-NT2RP3003354	0.66
NT2RP3003448	F-NT2RP3003448	0.61
NT2RP3003473	F-NT2RP3003473	0.94
NT2RP3003527	F-NT2RP3003527	0.94
NT2RP3003532	F-NT2RP3003532	0.93
NT2RP3003614	F-NT2RP3003614	0.81
NT2RP3003729	F-NT2RP3003729	0.90
NT2RP3003849	F-NT2RP3003849	0.93
NT2RP3003939	F-NT2RP3003939	0.67
NT2RP3004025	F-NT2RP3004025	0.83
NT2RP3004067	F-NT2RP3004067	0.74
NT2RP3004075	F-NT2RP3004075	0.77
NT2RP3004090	F-NT2RP3004090	0.94
NT2RP3004119	F-NT2RP3004119	0.57
NT2RP3004130	F-NT2RP3004130	0.66
NT2RP3004133	F-NT2RP3004133	0.94
NT2RP3004202	F-NT2RP3004202	0.53
NT2RP3004294	F-NT2RP3004294	0.71
NT2RP3004309	F-NT2RP3004309	0.92
NT2RP3004345	F-NT2RP3004345	0.73
NT2RP3004406	F-NT2RP3004406	0.62
NT2RP3004481	F-NT2RP3004481	0.76
NT2RP3004552	F-NT2RP3004552	0.78
NT2RP3004557	F-NT2RP3004557	0.78
NT2RP3004625	F-NT2RP3004625	0.87
NT2RP3004640	F-NT2RP3004640	0.82
NT2RP3004647	F-NT2RP3004647	0.94
NT2RP4000108	F-NT2RP4000108	0.94
NT2RP4000634	F-NT2RP4000634	0.69
NT2RP4000962	F-NT2RP4000962	0.67
NT2RP4001009	F-NT2RP4001009	0.56
NT2RP4001467	F-NT2RP4001467	0.94
NT2RP4001877	F-NT2RP4001877	0.94
NT2RP4001879	F-NT2RP4001879	0.82
NT2RP4002187	F-NT2RP4002187	0.7

Table 25 (continued)

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0.5 or higher.		
name of clone	name of sequence	maximal ATGpr1 score
NT2RP4002451	F-NT2RP4002451	0.53
NT2RP4002750	F-NT2RP4002750	0.67
OVARC1000003	F-OVARC1000003	0.62
OVARC1000105	F-OVARC1000105	0.62
OVARC1000137	F-OVARC1000137	0.72
OVARC1000255	F-OVARC1000255	0.78
OVARC1000307	F-OVARC1000307	0.94
OVARC1000313	F-OVARC1000313	0.94
OVARC1000331	F-OVARC1000331	0.57
OVARC1000410	F-OVARC1000410	0.79
OVARC1000467	F-OVARC1000467	0.83
OVARC1000529	F-OVARC1000529	0.94
OVARC1000553	F-OVARC1000553	0.94
OVARC1000873	F-OVARC1000873	0.88
OVARC1000916	F-OVARC1000916	0.94
OVARC1000956	F-OVARC1000956	0.92
OVARC1001030	F-OVARC1001030	0.94
OVARC1001049	F-OVARC1001049	0.94
OVARC1001086	F-OVARC1001086	0.73
OVARC1001132	F-OVARC1001132	0.94
OVARC1001163	F-OVARC1001163	0.75
OVARC1001222	F-OVARC1001222	0.67
OVARC1001336	F-OVARC1001336	0.92
OVARC1001338	F-OVARC1001338	0.89
OVARC1001570	F-OVARC1001570	0.94
OVARC1001607	F-OVARC1001607	0.86
OVARC1001725	F-OVARC1001725	0.81
OVARC1001952	F-OVARC1001952	0.66
OVARC1001991	F-OVARC1001991	0.94
OVARC1002058	F-OVARC1002058	0.79
PLACE1000442	F-PLACE1000442	0.93
PLACE1000740	F-PLACE1000740	0.57
PLACE1001016	F-PLACE1001016	0.92
PLACE1001114	F-PLACE1001114	0.94
PLACE1001123	F-PLACE1001123	0.89
PLACE1001231	F-PLACE1001231	0.81
PLACE1001340	F-PLACE1001340	0.77
PLACE1001401	F-PLACE1001401	0.87
PLACE1001407	F-PLACE1001407	0.94
PLACE1001464	F-PLACE1001464	0.91
PLACE1001500	F-PLACE1001500	0.77
PLACE1001516	F-PLACE1001516	0.89
PLACE1001564	F-PLACE1001564	0.52
PLACE1001655	F-PLACE1001655	0.56
PLACE1001795	F-PLACE1001795	0.91
PLACE1001836	F-PLACE1001836	0.81
PLACE1001918	F-PLACE1001918	0.76

Table 25 (continued)

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0.5 or higher.		
name of clone	name of sequence	maximal ATGpr1 score
PLACE1001949	F-PLACE1001949	0.94
PLACE1002080	F-PLACE1002080	0.76
PLACE1002095	F-PLACE1002095	0.61
PLACE1002153	F-PLACE1002153	0.94
PLACE1002329	F-PLACE1002329	0.94
PLACE1002355	F-PLACE1002355	0.57
PLACE1002374	F-PLACE1002374	0.92
PLACE1002547	F-PLACE1002547	0.87
PLACE1002726	F-PLACE1002726	0.83
PLACE1002905	F-PLACE1002905	0.94
PLACE1002911	F-PLACE1002911	0.73
PLACE1003135	F-PLACE1003135	0.69
PLACE1003163	F-PLACE1003163	0.61
PLACE1003428	F-PLACE1003428	0.61
PLACE1003438	F-PLACE1003438	0.93
PLACE1003460	F-PLACE1003460	0.94
PLACE1003573	F-PLACE1003573	0.78
PLACE1003598	F-PLACE1003598	0.57
PLACE1003644	F-PLACE1003644	0.93
PLACE1003737	F-PLACE1003737	0.88
PLACE1003772	F-PLACE1003772	0.80
PLACE1003852	F-PLACE1003852	0.82
PLACE1004078	F-PLACE1004078	0.94
PLACE1004166	F-PLACE1004166	0.92
PLACE1004168	F-PLACE1004168	0.58
PLACE1004279	F-PLACE1004279	0.64
PLACE1004441	F-PLACE1004441	0.90
PLACE1004450	F-PLACE1004450	0.85
PLACE1004482	F-PLACE1004482	0.57
PLACE1004492	F-PLACE1004492	0.85
PLACE1004519	F-PLACE1004519	0.74
PLACE1004520	F-PLACE1004520	0.94
PLACE1004630	F-PLACE1004630	0.76
PLACE1004648	F-PLACE1004648	0.59
PLACE1004816	F-PLACE1004816	0.94
PLACE1004887	F-PLACE1004887	0.94
PLACE1005003	F-PLACE1005003	0.80
PLACE1005031	F-PLACE1005031	0.88
PLACE1005239	F-PLACE1005239	0.94
PLACE1005383	F-PLACE1005383	0.52
PLACE1005426	F-PLACE1005426	0.52
PLACE1005519	F-PLACE1005519	0.69
PLACE1005544	F-PLACE1005544	0.59
PLACE1005569	F-PLACE1005569	0.68
PLACE1005682	F-PLACE1005682	0.64
PLACE1005736	F-PLACE1005736	0.67
PLACE1005815	F-PLACE1005815	0.94

Table 25 (continued)

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0.5 or higher.		
name of clone	name of sequence	maximal ATGpr1 score
PLACE1005878	F-PLACE1005878	0.92
PLACE1005927	F-PLACE1005927	0.94
PLACE1006073	F-FLACE1006073	0.94
PLACE1006208	F-PLACE1006208	0.75
PLACE1006277	F-PLACE1006277	0.65
PLACE1006290	F-PLACE1006290	0.94
PLACE1006443	F-PLACE1006443	0.89
PLACE1006716	F-PLACE1006716	0.63
PLACE1006959	F-PLACE1006959	0.89
PLACE1007028	F-PLACE1007028	0.94
PLACE1007081	F-PLACE1007081	0.77
PLACE1007096	F-PLACE1007096	0.84
PLACE1007702	F-PLACE1007702	0.51
PLACE1006282	F-PLACE1008282	0.70
PLACE1008297	F-PLACE1008297	0.64
PLACE1008469	F-PLACE1008469	0.94
PLACE1008549	F-PLACE1008549	0.52
PLACE1008657	F-PLACE1008657	0.94
PLACE1008716	F-PLACE1008716	0.79
PLACE1008744	F-PLACE1008744	0.94
PLACE1008984	F-PLACE1008984	0.74
PLACE1009279	F-PLACE1009279	0.60
PLACE1009527	F-PLACE1009527	0.87
PLACE1009546	F-PLACE1009546	0.80
PLACE1009600	F-PLACE1009600	0.76
PLACE1010011	F-PLACE1010011	0.94
PLACE1010078	F-PLACE1010078	0.86
PLACE1010081	F-PLACE1010081	0.92
PLACE1010251	F-PLACE1010251	0.62
PLACE1010445	F-PLACE1010445	0.94
PLACE1010713	F-PLACE1010713	0.62
PLACE1010827	F-PLACE1010827	0.88
PLACE1010968	F-PLACE1010968	0.51
PLACE1011045	F-PLACE1011045	0.64
PLACE1011116	F-PLACE1011116	0.69
PLACE1011181	F-PLACE1011181	0.78
PLACE1011236	F-PLACE1011236	0.66
PLACE1011364	F-PLACE1011364	0.94
PLACE1011407	F-PLACE1011407	0.64
PLACE1011516	F-PLACE1011516	0.83
PLACE1011708	F-PLACE1011708	0.94
PLACE1011824	F-PLACE1011824	0.94
PLACE3000181	F-PLACE3000181	0.74
SKNMC1000014	F-SKNMC1000014	0.76
SKNMC1000082	F-SKNMC1000082	0.74
THYRO1000196	F-THYRO1000196	0.71
THYRO1000400	F-THYRO1000400	0.73

Table 25 (continued)

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0.5 or higher.		
name of clone	name of sequence	maximal ATGpr1 score
THYRO1000584	F-THYRO1000584	0.73
THYRO1000678	F-THYRO1000678	0.86
THYRO1000776	F-THYRO1000776	0.91
THYRO1000795	F-THYRO1000795	0.92
THYRO1000846	F-THYRO1000846	0.78
THYRO1000866	F-THYRO1000866	0.56
THYRO1000956	F-THYRO1000956	0.94
THYRO1000964	F-THYRO1000964	0.80
THYRO1001063	F-THYRO1001063	0.87
THYRO1001071	F-THYRO1001071	0.94
THYRO1001102	F-THYRO1001102	0.90
THYRO1001113	F-THYRO1001113	0.74
THYRO1001128	F-THYRO1001128	0.79
THYRO1001205	F-THYRO1001205	0.94
THYRO1001242	F-THYRO1001242	0.94
THYRO1001266	F-THYRO1001266	0.94
THYRO1001456	F-THYRO1001456	0.69
THYRO1001457	F-THYRO1001457	0.88
THYRO1001471	F-THYRO1001471	0.91
THYRO1001478	F-THYRO1001478	0.89
THYRO1001529	F-THYRO1001529	0.55
THYRO1001593	F-THYRO1001593	0.94
THYRO1001608	F-THYRO1001608	0.94
THYRO1001641	F-THYRO1001641	0.94
THYRO1001700	F-THYRO1001700	0.76
THYRO1001702	F-THYRO1001702	0.80
THYRO1001770	F-THYRO1001770	0.73
THYRO1001803	F-THYRO1001803	0.94
Y79AA1000030	F-Y79AA1000030	0.88
Y79AA1000270	F-Y79AA1000270	0.63
Y79AA1000426	F-Y79AA1000426	0.92
Y79AA1000750	F-Y79AA1000750	0.94
Y79AA1000777	F-Y79AA1000777	0.94
Y79AA1000876	F-Y79AA1000876	0.94
Y79AA1000888	F-Y79AA1000888	0.85
Y79AA1000967	F-Y79AA1000967	0.92
Y79AA1001090	F-Y79AA1001090	0.74
Y79AA1001212	F-Y79AA1001212	0.93
Y79AA1001426	F-Y79AA1001426	0.82
Y79AA1001523	F-Y79AA1001523	0.94
Y79AA1001727	F-Y79AA1001727	0.94
Y79AA1001787	F-Y79AA1001787	0.75
Y79AA1001799	F-Y79AA1001799	0.60
Y79AA1001803	F-Y79AA1001803	0.68
Y79AA1002058	F-Y79AA1002058	0.89
Y79AA1002121	F-Y79AA1002121	0.66
Y79AA1002213	F-Y79AA1002213	0.86

Table 25 (continued)

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0.5 or higher.		
name of clone	name of sequence	maximal ATGpr1 score
Y79AA1002378	F-Y79AA1002378	0.82
Y79AA1002381	F-Y79AA1002381	0.89

Table 26

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0.3 or higher and less than 0.5.		
name of clone	name of sequence	maximal ATGpr1 score
HEMBA1000732	F-HEMBA1000732	0.32
HEMBA1001886	F-HEMBA1001886	0.46
HEMBA1002163	F-HEMBA1002163	0.44
HEMBA1002195	F-HEMBA1002195	0.41
HEMBA1003120	F-HEMBA1003120	0.44
HEMBA1004007	F-HEMBA1004007	0.31
HEMBA1004067	F-HEMBA1004067	0.49
HEMBA1005267	F-HEMBA1005267	0.37
HEMBA1006770	F-HEMBA1006770	0.40
HEMBB1000407	F-HEMBB1000407	0.41
HEMBB1000542	F-HEMBB1000542	0.47
HEMBB1002120	F-HEMBB1002120	0.33
MAMMA1000810	F-MAMMA1000810	0.43
MAMMA1001609	F-MAMMA1001609	0.32
MAMMA1001978	F-MAMMA1001978	0.32
MAMMA1002142	F-MAMMA1002142	0.34
MAMMA1002165	F-MAMMA1002165	0.34
NT2RM2001792	F-NT2RM2001792	0.37
NT2RM4001843	F-NT2RM4001843	0.44
NT2RP1000271	F-NT2RP1000271	0.41
NT2RP2000739	F-NT2RP2000739	0.39
NT2RP2001388	F-NT2RP2001388	0.47
NT2RP2001562	F-NT2RP2001562	0.41
NT2RP2001903	F-NT2RP2001903	0.46
NT2RP2003138	F-NT2RP2003138	0.41
NT2RP2003931	F-NT2RP2003931	0.44
NT2RP2004205	F-NT2RP2004205	0.37
NT2RP2005378	F-NT2RP2005378	0.43
NT2RP2005541	F-NT2RP2005541	0.31
NT2RP2006092	F-NT2RP2006092	0.47
NT2RP2006269	F-NT2RP2006269	0.41
NT2RP3000148	F-NT2RP3000148	0.44
NT2RP3000427	F-NT2RP3000427	0.38
NT2RP3000820	F-NT2RP3000820	0.44
NT2RP3001754	F-NT2RP3001754	0.30
NT2RP3001976	F-NT2RP3001976	0.46
NT2RP3002409	F-NT2RP3002409	0.31
NT2RP3002737	F-NT2RP3002737	0.33
NT2RP3003874	F-NT2RP3003874	0.34

Table 26 (continued)

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0.3 or higher and less than 0.5.		
name of clone	name of sequence	maximal ATGpr1 score
OVARC1000275	F-0VARC1000275	0.44
OVARC1000995	F-OVARC1000995	0.34
OVARC1001569	F-OVARC1001569	0.30
OVARC1001596	F-OVARC1001596	0.36
PLACE1000907	F-PLACE1000907	0.34
PLACE1002967	F-PLACE1002967	0.38
PLACE1003529	F-PLACE1003529	0.31
PLACE1006071	F-PLACE1006071	0.38
PLACE1006515	F-PLACE1006515	0.48
PLACE1007881	F-PLACE1007881	0.43
PLACE1008359	F-PLACE1008359	0.47
PLACE1008985	F-PLACE1008985	0.48
PLACE1009735	F-PLACE1009735	0.37
PLACE1010784	F-PLACE1010784	0.44
PLACE1011978	F-PLACE1011978	0.39
THYR01000061	F-THYR01000061	0.38
THYR01000580	F-THYR01000580	0.48
Y79AA1000127	F-Y79AA1000127	0.32
Y79AA1001272	F-Y79AA1001272	0.47
Y79AA1002129	F-Y79AA1002129	0.36

Table 27

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0 or higher and less than 0.3.		
name of clone	name of sequence	maximal ATGpr1 score
HEMBA1000006	F-HEMBA1000006	0.14
HEMBA1000875	F-HEMBA1000875	0.12
HEMBA1001296	F-HEMBA1001296	0.08
HEMBA1001563	F-HEMBA1001563	0.17
HEMBA1002227	F-HEMBA1002227	0.05
HEMBA1004952	F-HFMBA1004952	0.05
HEMBA1004971	F-HEMBA1004971	0.24
HEMBA1005230	F-HEMBA1005230	0.14
HEMBA1005246	F-HEMBA1005246	0.17
HEMBA1005913	F-HEMBA1005913	0.12
HEMBA1006912	F-HEMBA1006912	0.11
HEMBA1007063	F-HEMBA1007063	0.14
HEMBA1007291	F-HEMBA1007291	0.14
HEMBA1007332	F-HEMBA1007332	0.23
HEMBB1000309	F-HEMBB1000309	0.15
HEMBB1000567	F-HEMBB1000567	0.15
HEMBB1002039	F-HEMBB1002039	0.15
MAMMA1000528	F-MAMMA1000528	0.11
MAMMA1000614	F-MAMMA1000614	0.23
MAMMA1000706	F-MAMMA1000706	0.26
MAMMA1001066	F-MAMMA1001066	0.28

Table 27 (continued)

The clones selected by the keyword(s) of the top hit data in the SwissProt, and having the maximal score in the ATGpr1 0 or higher and less than 0.3.		
name of clone	name of sequence	maximal ATGpr1 score
MAMMA1001418	F-MAMMA1001418	0.12
MAMMA1001623	F-MAMMA1001623	0.23
NT2RM2000497	F-NT2RM2000497	0.17
NT2RM4000326	F-NT2RM4000326	0.23
NT2RM4000593	F-NT2RM4000593	0.16
NT2RM4000761	F-NT2RM4000761	0.13
NT2RP1000325	F-NT2RP1000325	0.29
NT2RP2000178	F-NT2RP2000178	0.28
NT2RP2000240	F-NT2RP2000240	0.16
NT2RP2000712	F-NT2RP2000712	0.15
NT2RP2001469	F-NT2RP2001469	0.28
NT2RP2001817	F-NT2RP2001817	0.15
NT2RP2002510	F-NT2RP2002510	0.26
NT2RP2002824	F-NT2RP2002824	0.14
NT2RP2002974	F-NT2RP2002974	0.05
NT2RP2003940	F-NT2RP2003940	0.25
NT2RP2003950	F-NT2RP2003950	0.07
NT2RP2005391	F-NT2RP2005391	0.19
NT2RP2006134	F-NT2RP2006134	0.10
NT2RP3000125	F-NT2RP3000125	0.26
NT2RP3000481	F-NT2RP3000481	0.11
NT2RP3000652	F-NT2RP3000652	0.24
NT2RP3000677	F-NT2RP3000677	0.11
NT2RP3001012	F-NT2RP3001012	0.22
NT2RP3001271	F-NT2RP3001271	0.29
NT2RP3001542	F-NT2RP3001542	0.28
OVARC1000090	F-OVARC1000090	0.21
OVARC1000439	F-OVARC1000439	0.21
OVARC1001260	F-OVARC1001260	0.10
OVARC1002178	F-OVARC1002178	0.12
PLACE1000033	F-PLACE1000033	0.20
PLACE1000258	F-PLACE1000258	0.21
PLACE1005539	F-PLACE1005539	0.27
PLACE1005745	F-PLACE1005745	0.29
PLACE1007077	F-PLACE1007077	0.21
PLACE1007296	F-PLACE1007296	0.27
PLACE1007591	F-PLACE1007591	0.20
PLACE1007845	F-PLACE1007845	0.21
PLACE2000118	F-PLACE2000118	0.23
PLACE3000213	F-PLACE3000213	0.21
PLACE4000354	F-PLACE4000354	0.20
Y79AA1000207	F-Y79AA1000207	0.21
Y79AA1001062	F-Y79AA1001062	0.28
Y79AA1001863	F-Y79AA1001863	0.15
Y79AA1002334	F-Y79AA1002334	0.23
Y79AA1002376	F-Y79AA1002376	0.29

EXAMPLE 13

Selection of cDNA clone NT2RP2036580

[0184] Clone NT2RP2006580 as well as clone HEMBA1000121 was selected from the representative sequences belonging to HRIFA000116a cluster of the most homologous sequence in the SwissProt with the keywoods "transmembrane". Although each of the clones, HEMBA1000121 and NT2RP2006580, was assembled with other clones for 5' extension, any other clones did not extend the clones toward the 5' direction. Accordingly, it is possible that both clones are full-length cDNA clones. The maximal ATGpr1 score of F-NT2RP2006580 is 0.37, and therefore, the fullness ratio is low. However, it is still possible for the sequence to cover the full-length.

[0185] Thus, the total number of selected clones is 830. Based on the top matching data resulted from Swiss-Prot homology search, 659 clones were selected. From them, 447 clones were selected by the keywords of "secretion" and "membrane". Among the clones selected based on the top matching data, 60 clones exhibited the maximal ATGpr1 score of 0.3 or higher and less than 0.5.

[0186] The sequences of F-NT2RP2006580 and R-NT2RP2006580 are shown in SEQ ID NO: 2545 and SEQ ID NO: 2546, respectively.

EXAMPLE 14

Full-length sequence analysis and homology search

[0187] Full-length sequence was determined for each selected cDNA clones. The nucleotide sequence determination was performed mainly by the dye-terminator method using custom synthesized DNA primers according to the primer walking procedure (custom synthesized DNA primers were used for sequencing; sequencing reaction was performed with DNA sequencing reagent supplied by PE Biosystems according to the supplier's manual; and the samples were analyzed in an automatic sequencer made by the same supplier). Sequence determination of some clones was carried out in the same manner but using a Licor DNA sequencer. Overlapping partial nucleotide sequences, which were obtained by the above-described method, were assembled together to determine a full-length nucleotide sequence. Amino acid sequences were then deduced from the determined full-length nucleotide sequences. However, amino acid sequence is not shown for a clone of which coding region was hard to be deduced or of which amino acid sequence has less than 100 amino acid residues. SEQ ID NOs corresponding to the respective clones are indicated in Table 370.

[0188] GenBank, Swiss-Prot and UniGene were searched for the determined nucleotide sequences by BLAST analysis. Matching data of cDNA clone which exhibits higher homology and of which functions are easily predicted based on the nucleotide sequences and the deduced amino acid sequences are selected from the BLAST analysis matching data with P value of 10^{-4} or less. The matching data selected are listed herein. However, there are some clones that did not match the criteria for judgment and such matching data of BLAST analysis are not shown herein. The results of homology search indicated in the last part of this specification are as follows.

[0189] Homology search result 1: data obtained by the homology search of Swiss-Prot database for representative sequences of the 5'-end cluster

[0190] Homology search result 2: homology of representative sequences of the 5'-end cluster to the data in Swiss-Prot database; the P value is 10^{-10} or less

[0191] Homology search result 3: homology of representative sequences of the 5'-end cluster to the data in Swiss-Prot database; the P value is higher than 10^{-10} and 10^{-4} or less

[0192] Homology search result 4: homology of representative sequences of the 5'-end cluster to the data in Swiss-Prot database; the P value is higher than 10^{-4} and 1 or less

[0193] Homology search result 5: data obtained by the homology search of Swiss-Prot database for 5'-end sequences of cDNA clone

[0194] Homology search result 6: data obtained by the homology search of GenBank database (http://www.ncbi.nlm.nih.gov/web/GenBank/) except for EST and STS sequence data for 5'-end sequences of cDNA clone

[0195] Homology search result 7: data obtained by the homology search of GenBank database (http://www.ncbi.nlm.nih.gov/web/GenBank/) except for EST and STS sequence data for 3'-end sequences of cDNA clone

[0196] Homology search result 8: data obtained by the homology search of Human UniGene database (http://www.ncbi.nlm.nih.gov/Unigene) for 5'-end sequences of cDNA clone

[0197] Homology search result 9: data obtained by the homology search of Human UniGene database (http://www.ncbi.nlm.nih.gov/Unigene) for 3'-end sequences of cDNA clone

[0198] Homology search result 10: result obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences

[0199] The P value indicates similarity between two sequences as a score by considering the probability that the two

sequences are accidentally similar. In general, as the value is lower, the similarity is higher. In general, as the value is lower, the homology is higher (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.L. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272).

Example 15. Gene expression analysis with hybridization using high density DNA filter

[0200] Nylon membrane for DNA spotting was prepared according to the following procedure. E. coli was cultured in each well of a 96-well plate (in a LB medium at 37. for 16 hours). A sample of each culture was suspended in 10 . 1 of sterile water in a well of a 96-well plate. The plate was heated at 100. for 10 minutes. Then, the boiled samples were analyzed by PCR. PCR was performed in a 20 .1 solution by using TaKaRa PCR Amplification Kit (Takara) according to the supplier's protocol. Primers used for the amplification of an insert cDNA in a plasmid were a pair of sequencing primers, ME761FW (5' tacggaagtgttacttctgc 3'/ SEQ ID NO: 3591) and ME1250RV (5' tgtgggaggttttttctcta 3'/ SEQ ID NO: 3592), or a pair of primers, M13M4 (5' gttttcccagtcacgac 3'/ SEQ ID NO: 3593) and M13RV (5' caggaaacagctatgac 3' / SEQ ID NO: 3594). PCR was performed using a thermal cycler, GeneAmp System 9600 (PE Biosystems) at 95. for 5 minutes; at 95. for 10 seconds and at 68. for 1 minute for 10 cycles; at 98. for 20 seconds and at 60. for 3 minutes for 20 cycles; and at 72. for 10 minutes. After the PCR, the 20 .1 reaction solution was loaded onto a 1% agarose gel and fractionated by electrophoresis. DNA on the gel was stained with ethidium bromide to confirm the amplification of cDNA. When cDNAs were not amplified by PCR, plasmids containing the corresponding insert cDNAs were prepared by the alkali-extraction method (J. Sambrook, E.F., Fritsh, & T. Maniatis, "Molecular Cloning, A laboratory manual/ 2nd edition, Cold Spring Harbor Laboratory Press, 1989).

[0201] Preparation of DNA array was carried out by the following procedure. A sample of a DNA solution was added in each well of a 384-well plate. DNA was spotted onto a nylon membrane (Boehringer) by using a 384-pin tool of Biomek 2000 Laboratory Automation System (Beckman-Coulter). Specifically, the 384-well plate containing the DNA was placed under the 384-pin tool. The independent 384 needles were simultaneously dipped into the DNA solution for DNA deposition. The needles were gently pressed onto a nylon membrane and the DNA deposited at the tips of needles was spotted onto the membrane. Denaturation of the spotted DNA and immobilization of the DNA on the nylon membrane were carried out according to standard methods (J. Sambrook, E.F., Fritsh, & T. Maniatis, "Molecular Cloning, A laboratory manual/ 2nd edition, Cold Spring Harbor Laboratory Press, 1989).

[0202] A probe for hybridization was radioisotope-labeled first strand cDNA. Synthesis of the first strand cDNA was performed by using Thermoscript(TM) RT-PCR System (GIBCO). Specifically, the first strand cDNA was synthesized by using 1.5 .g of mRNAs from various human tissues (Clontech), 1 .1 of 50.M Oligo(dT)20 and 50.Ci [.^{33}P]dATP according to an attached protocol. Purification of a probe was carried out by using ProbeQuant(TM) G-50 micro column (Amersham-Pharmacia Biotech) according to an attached protocol. In the next step, 2 units of E. coli RNase H were added to the reaction mixture. The mixture was incubated at room temperature for 10 minutes, and then, 100.g of human COT-1 DNA (GIBCO) was added thereto. The mixture was incubated at 97. for 10 minutes and then was allowed to stand on ice to give hybridization probe.

[0203] Hybridization of the radioisotope-labeled probe to the DNA array was performed according to standard methods (J. Sambrook, E.F., Fritsh, & T. Maniatis, Molecular Cloning, A laboratory manual/ 2nd edition, Cold Spring Harbor Laboratory Press, 1989). The membrane was washed as follows: the nylon membrane was washed 3 times by incubating it in Washing solution 1 (2xSSC, 1% SDS) at room temperature (about 26.) for 20 minutes; then the membrane was washed 3 times by incubating it in Washing solution 2 (0.1xSSC, 1% SDS) at 65. for 20 minutes.

[0204] Autoradiography was performed by using an image plate for BAS2000 (Fuji Photo Film Co., Ltd.). Specifically, the nylon membrane with probe hybridized thereon was wrapped with a piece of Saran Wrap and brought into tight contact with the image plate on the light-sensitive surface. The membrane with the image plate was placed in an imaging cassette for radioisotope and allowed to stand in dark place for 4 hours. The radioactivity recorded on the image plate was analyzed by using BAS2000 (Fuji Photo Film Co., Ltd.). The activity was subjected to electronic conversion and recorded as an image file of autoradiogram. The signal intensity of each DNA spot was analyzed by using Visage High Density Grid Analysis Systems (Genomic Solutions Inc.). The signal intensity was converted into numerical data. The data were taken in duplicate. The reproducibility was assessed by comparing the signal intensities of the corresponding spots on the duplicated DNA filters that were hybridized to a single DNA probe (Figure 2). In 95% of entire spots, the ratio between the corresponding spots falls within a range of 2 or less, and the correlation coefficient is r=1.97. Thus, the reproducibility is satisfactory.

[0205] The detection sensitivity in gene expression analysis was estimated by examining increases in the signal intensity of probe concentration-dependent spot in hybridization using a probe complementary to the DNA spotted on the nylon membrane. DNA used was PLACE 1008092 (the same as DNA deposited in GenBank under an Accession No. AF107253). The DNA array with DNA of PLACE1008092 was prepared according to the above-mentioned method. The probe used was prepared as follows: mRNA was synthesized in vitro from the clone, PLACE1008092. By using

this mRNA as a template, radioisotope-labeled first strand cDNA was synthesized in the same manner as described above, and the cDNA was used as the probe. In order to synthesize mRNA from PLACE1008092 in vitro, a plasmid in which the 5' end of the cDNA PLACE1008092 was ligated to the T7 promoter of pBluescript SK(-) was constructed. Specifically, the PLACE1008092 insert was cut out from pME18SFL3 carrying the cDNA at a DraIII site thereof by XhoI digestion. The resulting PLACE1008092 fragment was ligated to XhoI-predigested pBluescript SK(-) by using DNA ligation kit ver.2 (Takara). The in vitro mRNA synthesis from PLACE1008092 inserted into pBluescript SK(-) was carried out by using Ampliscribe(TM) T7 high yield transcription kit (Epicentre technologies). Hybridization and the analysis of signal intensity of each DNA spot were performed by the same methods as described above. When the probe concentration is $1x10^7$.g/ml or less, there was no increase of signal intensity proportional to the probe concentration. Therefore, it was assumed to be difficult to compare the signals with one another in this concentration range. Thus, the spots with the intensity of 40 or less were uniformly taken as low level signals (Figure 3). Within a concentration of the probe ranging from $1x10^7$.g/ml to 0.1.g/ml, the signal was found to increase in a probe concentration-dependent manner. The detection limit represented as the ratio of the expression level of test mRNA to that of total mRNA in a sample was 1:100,000.

[0206] Tables 28-184 (also containing clones without description in Examples) show the expression of each cDNA in human normal tissues (heart, lung, pituitary gland, thymus, brain, kidney, liver and spleen). The expression levels are indicated with numerical values of 0-10,000. Genes that were expressed in at least a single tissue are indicated below by the corresponding clone names:

clone: BNGH41000020, BNGH41000087, BNGH41000091, HEMBA1000121, HEMBA1000275, HEMBA1000300, HEMBA1000443, HEMBA1000462, HEMBA1000477, HEMBA1000634, HEMBA1000713, HEMBA1000835, HEMBA1000875, HEMBA1000940, HEMBA1000962, HEMBA1001228, HEMBA1001296, HEMBA1001390, HEMBA1001563, HEMBA1001621, HEMBA1002048, HEMBA1002131, HEMBA1002163, HEMBA1002164, HEMBA1002167, HEMBA1002178, HEMBA1002195, HEMBA1002227, HEMBA1002239, HEMBA1002316, HEMBA1002421, HEMBA1002524, HEMBA1002551, HEMBA1002767, HEMBA1002985, HEMBA1002992, HEMBA1003047, HEMBA1003072, HEMBA1003101, HEMBA1003120, HEMBA1003230, HEMBA1003294, HEMBA1003315, HEMBA1003392, HEMBA1003399, HEMBA1003487, HEMBA1003530, HEMBA1003945, HEMBA1004007, HEMBA1004067, HEMBA1001085, HEMBA1004110, HEMBA1004391, HEMBA1004444, HEMBA1004454, HEMBA1004505, HEMBA1004797, HEMBA1004952, HEMBA1005070, HEMBA1005084, HEMBA1005145, HEMBA1005230, HEMBA1005246, HEMBA1005337, HEMBA1005430, HEMBA1005449, HEMBA1005489, HEMBA1005545, HEMBA1005698, HEMBA1005929, HEMBA1005945, HEMBA1005016, HEMBA1006171, HEMBA1006276, HEMBA1006311, HEMBA1006335, HEMBA1006357, HEMBA1006430, HEMBA1006482, HEMBA1006517, HEMBA1006544, HEMBA1006658, HEMBA1006707, HEMBA1006749, HEMBA1006770, HEMBA1006902, HEMBA1006912, HEMBA1006916, HEMBA1006960, HEMBA1007013, HEMBA1007057, HEMBA1007063, HEMBA1007291, HEMBA1007332, HEMBB1000106, HEMBB1000309, HEMBB1000447, HEMBB1000542, HEMBB1000567, HEMBB1000642, HEMBB1000905, HEMBB1001026, HEMBB1001048, HEMBB1001407, HEMBB1001530, HEMBB1001573, HEMBB1001847, HEMBB1001959, HEMBB1001978, HEMBB1002039, HEMBB1002041, HEMBB1002051, HEMBB1002162, HEMBB1002228, HEMBB1002302, HEMBB1002427, HEMBB1002465, HEMBB1002661, HEMBB1002663, HEMBB1002693, MAMMA1000046, MAMMA1000102, MAMMA1000106, MAMMA1000118, MAMMA1000204, MAMMA1000226, MAMMA1000403, MAMMA1000449, MAMMA1000457, MAMMA1000473, MAMMA1000528, MAMMA1000591, MAMMA1000614, MAMMA1000652, MAMMA1000681, MAMMA1000706, MAMMA1000788, MAMMA1000810, MAMMA1000814, MAMMA1000881, MAMMA1000986, MAMMA1000994, MAMMA1001043, MAMMA1001066, MAMMA1001094, MAMMA1001141, MAMMA1001150, MAMMA1001284, MAMMA1001310, MAMMA1001344, MAMMA1001418, MAMMA1001532, MAMMA1001609, MAMMA1001615, MAMMA1001634, MAMMA1001893, MAMMA1001901, MAMMA1001957, MAMMA1002070, MAMMA1002091, MAMMA1002095, MAMMA1002128, MAMMA1002142, MAMMA1002165, MAMMA1002205, MAMMA1002224, MAMMA1002586, MAMMA1003126, NT2RM1000407, NT2RM1000462, NT2RM1000542, NT2RM1000789, NT2RM1000855, NT2RM1000858, NT2RM2000241, NT2RM2000306, NT2RM2000410, NT2RM2000423, NT2RM2000497, NT2RM2000514, NT2RM2000565, NT2RM2000582, NT2RM2000589, NT2RM2000622, NT2RM2000773, NT2RM2001126, NT2RM2001626, NT2RM2001792, NT2RM2001941, NT2RM4000198, NT2RM4000295, NT2RM4000444, NT2RM4000593, NT2RM4000761, NT2RM4000965, NT2RM4000997, NT2RM4001321, NT2RM4001325, NT2RM4001377, NT2RM4001735, NT2RM4001768, NT2RM4001843, NT2RP1000002, NT2RP1000181, NT2RP1000271, NT2RP1000300, NT2RP1000325, NT2RP1000465, NT2RP1000468, NT2RP1000740, NT2RP1000903, NT2RF1000981, NT2RP2000092, NT2RP2000178, NT2RP2000240, NT2RP2000447, NT2RP2000479, NT2RP2000533, NT2RP2000610, NT2RP2000616, NT2RP2000694, NT2RP2000739, NT2RP2001200, NT2RP2001223, NT2RP2001388, NT2RP2001469, NT2RP2001480, NT2RP2001514, NT2RP2001529, NT2RP2001538, NT2RP2001562, NT2RP2001662, NT2RP2001878, NT2RP2001903,

NT2RP2001921, NT2RP2001956, NT2RP2002015, NT2RP2002063, NT2RP2002188, NT2RP2002232,
NT2RP2002409, NT2RP2002510, NT2RP2002527, NT2RP2002533, NT2RP2002564, NT2RP2002721,
NT2RP2002824, NT2RP2002942, NT2RP2002974, NT2RP2003138, NT2RP2003179, NT2RP2003210,
NT2RP2003302, NT2RP2003369, NT2RP2003383, NT2RP2003390, NT2RP2003469, NT2RP2003593,
NT2RP2003599, NT2RP2003655, NT2RP2003940, NT2RP2003950, NT2RP2004069, NT2RP2004108,
NT2RP2004141, NT2RP2004179, NT2RP2004205, NT2RP2004447, NT2RP2004524, NT2RP2004556,
NT2RP2004606, NT2RP2004648, NT2RP2004794, NT2RP2004837, NT2RP2004847, NT2RP2005027,
NT2RP2005069, NT2RP2005163, NT2RP2005181, NT2RP2005247, NT2RP2005378, NT2RP2005391,
NT2RP2005425, NT2RP2005463, NT2RP2005535, NT2RP2005541, NT2RP2005597, NT2RP2005632,
NT2RP2005666, NT2RP2005774, NT2RP2005878, NT2RP2005887, NT2RP2005941, NT2RP2006004,
NT2RP2006042, NT2RP2006092, NT2RP2006099, NT2RP2006269, NT2RP3000011, NT2RP3000022,
NT2RP3000059, NT2RP3000063, NT2RP3000125, NT2RP3000148, NT2RP3000171, NT2RP3000172,
NT2RP3000201, NT2RP3000232, NT2RP3000304, NT2RP3000378, NT2RP3000436, NT2RP3000460,
NT2RP3000645, NT2RP3000652, NT2RP3000676, NT2RP3000677, NT2RP3000721, NT2RP3000789,
NT2RP3000818, NT2RP3000820, NT2RP3000838, NT2RP3000907, NT2RP3000921, NT2RP3001044,
NT2RP3001159, NT2RP3001170, NT2RP3001195, NT2RP3001271, NT2RP3001388, NT2RP3001560,
NT2RP3001592, NT2RP3001685, NT2RP3001738, NT2RP3001754, NT2RP3001858, NT2RP3001976,
NT2RP3002015, NT2RP3002160, NT2RP3002281, NT2RP3002311, NT2RP3002324, NT2RP3002353,
NT2RP3002409, NT2RP3002411, NT2RP3002721, NT2RP3002737, NT2RP3002738, NT2RP3002836,
NT2RP3002900, NT2RP3002958, NT2RP3003000, NT2RP3003076, NT2RP3003354, NT2RP3003448,
NT2RP3003469, NT2RP3003473, NT2RP3003532, NT2RP3003614, NT2RP3003729, NT2RP3003849,
NT2RP3003874, NT2RP3003939, NT2RP3003963, NT2RP3004025, NT2RP3004067, NT2RP3004083,
NT2RP3004090, NT2RP3004119, NT2RP3004130, NT2RP3004133, NT2RP3004202, NT2RP3004294,
NT2RP3004309, NT2RP3004321, NT2RP3004355, NT2RP3004374, NT2RP3004406, NT2RP3004481,
NT2RP3004552, NT2RP3004557, NT2RP3004625, NT2RP3004640, NT2RP3004647, NT2RP4000108,
NT2RP4000634, NT2RP4001877, NT2RP4001879, NT2RP4002187, NT2RP4002715, NT2RP4002750,
OVARC1000090, OVARC1000105, OVARC1000137, OVARC1000208, OVARC1000255, OVARC1000313,
OVARC1000331, OVARC1000410, OVARC1000439, OVARC1000467, OVARC1000529, OVARC1000553,
OVARC1000775, OVARC1000853, OVARC1000873, OVARC1000916, OVARC1000956, OVARC1000995,
OVARC1001030, OVARC1001049, OVARC1001086, OVARC1001163, OVARC1001260, OVARC1001336,
OVARC1001569, OVARC1001570, OVARC1001596, OVARC1001807, OVARC1001833, OVARC1001991,
PLACE1000231, PLACE1000258, PLACE1000442, PLACE1000560, PLACE1000912, PLACE1000927,
PLACE1001016, PLACE1001100, PLACE1001114, PLACE1001183, PLACE1001229, PLACE1001340,
PLACE1001407, PLACE1001500, PLACE1001516, PLACE1001655, PLACE1001836, PLACE1001918,
PLACE1002080, PLACE1002095, PLACE1002153, PLACE1002329, PLACE1002374, PLACE1002518,
PLACE1002547, PLACE1002726, PLACE1002905, PLACE1002911, PLACE1002967, PLACE1003163,
PLACE1003407, PLACE1003428, PLACE1003438, PLACE1003460, PLACE1003529, FLACE1003598,
PLACE1003644, PLACE1003772, PLACE1003839, PLACE1003845, PLACE1003852, PLACE1004078,
PLACE1004166, PLACE1004168, PLACE1004199, PLACE1004279, PLACE1004282, PLACE1004305,
PLACE1004441, PLACE1004482, PLACE1004492, PLACE1004520, PLACE1004630, PLACE1004637,
PLACE1004648, PLACE1004816, PLACE1004887, PLACE1005005, PLACE1005031, PLACE1005383,
PLACE1005410, PLACE1005426, PLACE1005539, PLACE1005544, PLACE1005569, PLACE1005725,
PLACE1005736, PLACE1005768, PLACE1005815, PLACE1005878, PLACE1005927, PLACE1006071,
PLACE1006073, PLACE1006079, PLACE1006277, PLACE1006443, PLACE1006716, PLACE1006809,
PLACE1007077, PLACE1007096, PLACE1007626, PLACE1007702, PLACE1008469, PLACE1008985,
PLACE1009067, PLACE1009527, PLACE1009982, PLACE1010078, PLACE1010251, PLACE1010445,
PLACE1011045, PLACE1011116, PLACE1011181, PLACE1011236, PLACE1011364, PLACE1011516,
PLACE1011708, PLACE1011978, PLACE2000118, PLACE2000219, PLACE3000181, PLACE4000354,
PLACE4000455, SKNMC1000014, THYRO1000061, THYRO1000099, THYRO1000584, THYRO1000795,
THYRO1000866, THYRO1000999, THYRO1001063, THYRO1001113, THYRO1001128, THYRO1001205,
THYRO1001237, THYRO1001242, THYRO1001456, THYRO1001457, THYRO1001478, THYRO1001495,
THYRO1001523, THYRO1001529, THYRO1001593, THYRO1001608, THYRO1001700, THYRO1001702,
THYRO1001725, THYRO1001770, THYRO1001803, Y79AA1000127, Y79AA1000207, Y79AA1000226,
Y79AA1000270, Y79AA1000426, Y79AA1000521, Y79AA1000776, Y79AA1000777, Y79AA1000888,
Y79AA1000967, Y79AA1001013, Y79AA1001090, Y79AA1001272, Y79AA1001328, Y79AA1001426,
Y79AA1001427, Y79AA1001430, Y79AA1001523, Y79AA1001530, Y79AA1001592, Y79AA1001727,
Y79AA1001787, Y79AA1001793, Y79AA1001799, Y79AA1001803, Y79AA1001863, Y79AA1002022,
Y79AA1002213, Y79AA1002373, Y79AA1002376, Y79AA1002381.

[0207] Genes that were expressed in all the tissues tested are indicated below by the corresponding clone names: clone: BNGH41000020, HEMBA1000300, HEMBA1001390, HEMBA1002239, HEMBA1002316, HEMBA1004007, HEMBA1004067, HEMBA1005145, HEMBA1005230, HEMBA1005929, HEMBA1006357, HEMBA1006482, HEMBB1000567, HEMBB1001847, NEMBB1001978, MAMMA1000614, MAMMA1000652, MAMMA1000810, MAMMA1000814, MAMMA1001066, MAMMA1001094, MAMMA1001284, MAMMA1001310, MAMMA1001634, MAMMA1002165, MAMMA1002205, MAMMA1002224, NT2RM1000462, NT2RM1000855, NT2RM1000858, NT2RM2000423, NT2RM4000761, NT2RM4000997, NT2RP1000271, NT2RP1000325, NT2RP1000465, NT2RP2001538, NT2RP2001662, NT2RP2001903, NT2RP2002015, NT2RP2002188, NT2RP2002409, NT2RP2002510, NT2RP2002533, NT2RP2004556, NT2RP2004794, NT2RP2004847, NT2RP2005069, NT2RP2005163, NT2RP2005535, NT2RP2006269, NT2RP3000171, NT2RP3000645, NT2RP3000838, NT2RP3001271, NT2RP3001754, NT2RP3003076, NT2RP3003354, NT2RP3003614, NT2RP3004640, NT2RP3004647, OVARC1000090, OVARC1000208, OVARC1000553, OVARC1000995, OVARC1001030, OVARC1001049, PLACE1000231, PLACE1000258, PLACE1001516, PLACE1002080, PLACE1002911, PLACE1003598, PLACE1004648, PLACE1006443, PLACE1008469, PLACE1011708, PLACE2000118, THYRO1001128, THYRO1001205, THYRO1001242, THYRO1001803, Y79AA1000207, Y79AA1001013, Y79AA1001272, Y79AA1001328, Y79AA1001793, Y79AA1001863, Y79AA1002022, Y79AA1002376.

[0208] Genes that were expressed at low levels in any of the tissues tested are indicated below by the corresponding clone names: clone: HEMBA1000006, HEMBA1000128, HEMBA1000349, HEMBA1000590, HEMBA1000671, HEMBA1000732, HEMBA1000745, HEMBA1000907, HEMBA1001184, HEMBA1001221, HEMBA1001272, HEMBA1001297, HEMBA1001878, HEMBA1001886, HEMBA1002420, HEMBA1003497, HEMBA1003602, HEMBA1003732, HEMBA1004250, HEMBA1004785, HEMBA1004971, HEMBA1004982, HEMBA1005267, HEMBA1005522, HEMBA1005913, HEMBA1006299, HEMBA1006572, HEMBA1006724, HEMBA1007241, HEMBB1000276, HEMBB1000407, HEMBB1000668, HEMBB1000679, HEMBB1000881, HEMBB1001200, HEMBB1001547, HEMBB1002120, HEMBB1002245, MAMMA1000141, MAMMA1000496, MAMMA1001237, MAMMA1001623, MAMMA1001978, MAMMA1002080, MAMMA1002087, MAMMA1002234, MAMMA1002633, NT2RM1000580, NT2RM1000899, NT2RM2000632, NT2RM2001643, NT2PM2001818, NT2RM2001902, NT2RM2001939, NT2RM4000100, NT2RM4000115, NT2RM4000284, NT2RM4000326, NT2RM4000417, NT2RM4000587, NT2RM4000648, NT2RM4002352, NT2RP1000050, NT2RP1000239, NT2RP1000261, NT2RP1000448, NT2RP1000551, NT2RP1000579, NT2RP1000613, NT2RP1000679, NT2RP1001004, NT2RP1001020, NT2RP1001031, NT2RP1001563, NT2RP2000394, NT2RP2000514, NT2RP2000649, NT2RP2000663, NT2RP2000712, NT2RP2000818, NT2RP2000903, NT2RP2001276, NT2RP2001495, NT2RP2001755, NT2RP2001769, NT2RP2001817, NT2RP2001915, NT2RP2001948, NT2RP2002304, NT2RP2002674, NT2RP2002976, NT2RP2003042, NT2RP2003545, NT2RP2003664, NT2RP2003931, NT2RP2004495, NT2RP2004670, NT2RP2005514, NT2RP2005883, NT2RP2005994, NT2RP2006134, NT2RP2006512, NT2RP3000169, NT2RP3000444, NT2RP3000481, NT2RP3000616, NT2RP3000871, NT2RP3001012, NT2RP3001061, NT2RP3001240, NT2RP3001322, NT2RP3001542, NT2RP3002286, NT2RP3002342, NT2RP3002448, NT2RP3002571, NT2RP3002664, NT2RP3002790, NT2RP3002887, NT2RP3002983, NT2RP3003527, NT2RP3003535, NT2RP3003559, NT2RP3004000, NT2RP3004075, NT2RP3004345, NT2RP4000962, NT2RP4001001, NT2RP4001009, NT2RP4001467, NT2RP4002451, OVARC1000003, OVARC1000275, OVARC1000298, OVARC1000307, OVARC1000811, OVARC1001132, OVARC1001222, OVARC1001338, OVARC1001607, OVARC1001725, OVARC1001727, OVARC1002058, OVARC1002178, PLACE1000033, PLACE1000740, PLACE1000914, PLACE1000986, PLACE1001123, PLACE1001231, PLACE1001401, PLACE1001464, PLACE1001536, PLACE1001564, PLACE1001788, PLACE1001795, PLACE1001949, PLACE1002355, PLACE1003135, PLACE1003573, PLACE1003737, PLACE1004028, PLACE1004450, PLACE1004519, PLACE1005003, PLACE1005239, PLACE1005250, PLACE1005519, PLACE1005601, PLACE1005660, PLACE1005669, PLACE1005682, PLACE1005745, PLACE1006093, PLACE1006208, PLACE1006219, PLACE1006290, PLACE1006515, PLACE1006786, PLACE1006959, PLACE1007028, PLACE1007040, PLACE1007081, PLACE1007296, PLACE1007591, PLACE1007845, PLACE1007881, PLACE1007971, PLACE1008282, PLACE1008297, PLACE1008359, PLACE1008549, PLACE1008657, PLACE1008716, PLACE1008744, PLACE1008984, PLACE1009196, PLACE1009279, PLACE1009546, PLACE1009600, PLACE1009735, PLACE1010011, PLACE1010081, PLACE1010713, PLACE1010784, PLACE1010827, PLACE1010968, PLACE1011407, PLACE1011824, PLACE3000213, SKNMC1000004, SKNMC1000082, THYRO1000036, THYRO1000196, THYRO1000400, THYRO1000580, THYRO1000678, THYRO1000776, THYRO1000846, THYRO1000956, THYRO1001071, THYRO1001102, THYRO1001266, THYRO1001327, THYRO1001471, Y79AA1000876, Y79AA1000959, Y79AA1001056, Y79AA1001062, Y79AA1001264, Y79AA1001795.

[0209] Genes exhibiting characteristic features in the expression thereof were selected by statistical analysis of these

data. Two examples are shown below to describe the selection of genes of which expression is varied greatly among tissues. The .-actin gene is used frequently as a control in gene expression analysis. Genes of which expression is varied greatly among tissues as compared that of the .-actin gene were determined as follows. Specifically, sum of squared deviation was calculated in the signal intensity of .-actin observed in each tissue, which was divided by 7 degrees of freedom to determine a variance S_a^2. Next, sum of squared deviation was calculated in the signal intensity of a compared gene in each tissue, which was divided by 7 degrees of freedom to determine a variance S_b^2. By taking variance ratio F as $F=S_b^2/S_a^2$, genes with a significance level of 5% or more were extracted in the F distribution. Genes extracted are indicated below by the corresponding clone names: clone: BNGH41000020, NT2RM4000761, Y79AA1002376.

[0210] Gene of OVARC1000037{heterogeneous nuclear ribonucleoprotein (hnRNP)} which expression is varied little. Genes of which expression is varied greatly among tissues as compared that of the OVARC1000037 gene were determined as follows. Specifically, sum of squared deviation was calculated in the signal intensity of .-actin observed in each tissue, which was divided by 7 degrees of freedom to determine a variance S_a^2. Next, sum of squared deviation was calculated in the signal intensity of a gene to be compared observed in each tissue, which was divided by 7 degrees of freedom to determine a variance S_b^2. By taking variance ratio F as $F=S_b^2/S_a^2$, genes with a significance level of 5% or more were extracted in the F distribution. Genes extracted are indicated below by the corresponding clone names: clone: BNGH41000020, HEMBA1000300, OVARC1001030, NT2RM4000761, PLACE1000231, HEMBA1002316, NT2RP1000325, NT2RP1000271, PLACE1004648, HEMBA1005145, HEMBA1005929, NT2RP2002510, NT2RP2001538, NT2RP2002409, NT2RP2002188, NT2RP2001903, NT2RP2002533, NT2RP2002015, NT2RP2006269, NT2RP2004837, NT2RP2004205, NT2RP2005378, HEMBA1006357, HEMBB1000567, NT2RP2003940, NT2RP2004794, HEMBA1006912, NT2RP2004556, NT2RP2005163, NT2RP3000838, NT2RP3001271, PLACE2000118, NT2RP3000645, NT2RP3003076, HEMBB1002693, MAMMA1000046, NT2RP3003354, THYR01001205, MAMMA1000614, MAMMA1000652, MAMMA1000810, THYRO1001242, MAMMA1001066, MAMMA1002224, MAMMA1001634, MAMMA1001094, MAMMA1002205, NT2RM1000855, NT2RM1000858, Y79AA1002376, NT2RM2000423.

[0211] Thus, characteristic features in the expression of a gene are illustrated by comparing and statistically analyzing the expression of many genes.

Analysis of disease-associated genes

[0212] Non-enzymic protein glycation reaction is believed to be a cause of a variety of chronic diabetic complications. Accordingly, genes of which expression is elevated or decreased in a glycated protein-specific manner in the endothelial cells are associated with diabetic complications caused by glycated proteins. Vascular endothelial cells are affected with glycated proteins present in blood. Reaction products of non-enzymic protein glycation include amadori compound (glycated protein) as a mildly glycated protein and advanced glycation endproduct as a heavily glycated protein. Hence, a survey was carried out for genes of which expression levels are varied depending on the presence of these glycated proteins in endothelial cells. The mRNAs were extracted from endothelial cells that were cultured in the presence or absence of glycated protein. The mRNAs were converted into radiolabeled first strand cDNAs for preparing probes. The probes were hybridized to the above-mentioned DNA array. Signal of each DNA spot was detected by BAS2000 and analyzed by ArrayGauge (Fuji Photo Film Co., Ltd.).

[0213] Advanced glycation endproduct of bovine serum albumin was prepared as follows: bovine serum albumin (BSA; Sigma) was incubated in a phosphate buffer solution containing 50 mM glucose at 37 for 8 weeks; and the resulting brownish BSA was dialyzed against a phosphate buffer solution.

[0214] Human normal pulmonary arterial endothelial cells (Cell Applications) were cultured in an Endothelial Cell Growth Medium (Cell Applications). The culture dish (Farcon) with the cells were incubated in a CO_2 incubator (37., 5% CO_2, in a humid atmosphere). When the cells were grown to be confluent in the dish, 250.g/ml of bovine serum albumin (sigma), glycated bovine serum albumin (Sigma) or advanced glycation endproduct of bovine serum albumin was added thereto and the cells were incubated for 33 hours. The mRNA was extracted from the cells by using a FastTack(TM) 2.0 kit (Invitrogen). The labeling of hybridization probe was carried out by using the mRNA according to the same procedure as described above.

[0215] Table 185 shows the expression level of each cDNA in human pulmonary arterial endothelial cells cultured in a medium containing bovine serum albumin (sigma), glycated bovine serum albumin (Sigma) or advanced glycation endproduct of bovine serum albumin. Genes of which expression was detected in the endothelial cell are as follows: BNGH41000020, BNGH41000087, HEMBA1000275, HEMBA1000300, HEMBA1000477, HEMBA1000634, HEMBA1000671, HEMBA1000713, HEMBA1000745, HEMBA1000835, HEMBA1000875, HEMBA1000940, HEMBA1001390, HEMBA1002131, HEMBA1002163, HEMBA1002164, HEMBA1002195, HEMBA1002227, HEMBA1002239, HEMBA1002420, HEMBA1002767, HEMBA1002992, HEMBA1003047, HEMBA1003120, HEMBA1003294, HEMBA1003315, HEMBA1003602, HEMBA1003945, HEMBA1004007, HEMBA1004067,

HEMBA1004971, HEMBA1005145, HEMBA1005267, HEMBA1005337, HEMBA1005698, HEMBA1005929, HEMBA1005945, HEMBA1006171, HEMBA1006299, HEMBA1006335, HEMBA1006357, HEMBA1006430, HEMBA1006482, HEMBA1006658, HEMBA1006724, HEMBA1006770, HEMBA1006912, HEMBA1006960, HEMBA1007063, HEMBB1000447, HEMBB1000642, HEMBB1000905, HEMBB1001026, HEMBB1001048, HEMBB1001573, HEMBB1001847, HEMBB1001978, HEMBB1002041, HEMBB1002427, HEMBB1002663, HEMBB1002693, MAMMA1000102, MAMMA1000106, MAMMA1000204, MAMMA1000403, MAMMA1000449, MAMMA1000614, MAMMA1000652, MAMMA1000810, MAMMA1000814, MAMMA1000881, MAMMA1000986, MAMMA1001066, MAMMA1001237, MAMMA1001284, MAMMA1001344, MAMMA1001615, MAMMA1001634, MAMMA1001893, MAMMA1001901, MAMMA1001957, MAMMA1002087, MAMMA1002095, MAMMA1002165, MAMMA1002205, MAMMA1002224, MAMMA1002633, MAMMA1003126, NT2RM1000462, NT2RM1000580, NT2RM1000789, NT2RM1000855, NT2RM1000858, NT2RM2000241, NT2RM2000306, NT2RM2000410, NT2RM2000423, NT2RM2000582, NT2RM2000589, NT2RM2000622, NT2RM2000773, NT2RM4000100, NT2RM4000198, NT2RM4000284, NT2RM4000444, NT2RM4000587, NT2RM4000593, NT2RM4000761, NT2RM4000997, NT2RM4001321, NT2RM4001325, NT2RM4001377, NT2RM4001735, NT2RM4001768, NT2RM4001843, NT2RP1000002, NT2RP1000181, NT2RP1000271, NT2RP1000300, NT2RP1000325, NT2RP1000465, NT2RP1000740, NT2RP1000981, NT2RP2000092, NT2RP2000240, NT2RP2000479, NT2RP2000533, NT2RP2000610, NT2RP2000616, NT2RP2000649, NT2RP2000663, NT2RP2000712, NT2RP2000903, NT2RP2001276, NT2RP2001388, NT2RP2001480, NT2RP2001495, NT2RP2001529, NT2RP2001538, NT2RP2001662, NT2RP2001878, NT2RP2001903, NT2RP2001948, NT2RP2001956, NT2RP2002015, NT2RP2002188, NT2RP2002232, NT2RP2002409, NT2RP2002510, NT2RP2002527, NT2RP2002533, NT2RP2002564, NT2RP2002721, NT2RP2002824, NT2RP2002942, NT2RP2002976, NT2RP2003138, NT2RP2003210, NT2RP2003390, NT2RP2003593, NT2RP2003599, NT2RP2003664, NT2RP2003931, NT2RP2003940, NT2RP2004069, NT2RP2004108, NT2RP2004179, NT2RP2004205, NT2RP2004495, NT2RP2004524, NT2RP2004556, NT2RP2004606, NT2RP2004648, NT2RP2004794, NT2RP2004837, NT2RP2004847, NT2RP2005027, NT2RP2005069, NT2RP2005163, NT2RP2005247, NT2RP2005378, NT2RP2005425, NT2RP2005535, NT2RP2005541, NT2RP2005632, NT2RP2005774, NT2RP2005878, NT2RP2006099, NT2RP2006134, NT2RP2006269, NT2RP2006512, NT2RP3000011, NT2RP3000171, NT2RP3000201, NT2RP3000232, NT2RP3000436, NT2RP3000460, NT2RP3000645, NT2RP3000652, NT2RP3000676, NT2RP3000721, NT2RP3000818, NT2RP3000820, NT2RP3000838, NT2RP3000907, NT2RP3001159, NT2RP3001195, NT2RP3001240, NT2RP3001271, NT2RP3001388, NT2RP3001592, NT2RP3001738, NT2RP3001754, NT2RP3002015, NT2RP3002324, NT2RP3002342, NT2RP3002353, NT2RP3002409, NT2RP3002448, NT2RP3002721, NT2RP3002737, NT2RP3002738, NT2RP3002836, NT2RP3002900, NT2RP3003076, NT2RP3003354, NT2RP3003448, NT2RP3003473, NT2RP3003532, NT2RP3003614, NT2RP3003939, NT2RP3003963, NT2RP3004025, NT2RP3004067, NT2RP3004075, NT2RP3004083, NT2RP3004090, NT2RP3004119, NT2RP3004130, NT2RP3004133, NT2RP3004294, NT2RP3004309, NT2RP3004345, NT2RP3004374, NT2RP3004557, NT2RP3004625, NT2RP3004640, NT2RP3004647, NT2RP4000108, NT2RP4000634, NT2RP4001001, NT2RP4001009, NT2RP4001467, NT2RP4001877, NT2RP4001879, NT2RP4002187, NT2RP4002451, NT2RP4002715, OVARC1000003, OVARC1000090, OVARC1000105, OVARC1000137, OVARC1000208, OVARC1000298, OVARC1000313, OVARC1000331, OVARC1000410, OVARC1000439, OVARC1000553, OVARC1000775, OVARC1000853, OVARC1000873, OVARC1000916, OVARC1000956, OVARC1000995, OVARC1001030, OVARC1001049, OVARC1001086, OVARC1001132, OVARC1001222, OVARC1001260, OVARC1001336, OVARC1001569, OVARC1001570, OVARC1001596, OVARC1001607, OVARC1001807, OVARC1001991, PLACE1000231, PLACE1000258, PLACE1000442, PLACE1000740, PLACE1000927, PLACE1001016, PLACE1001100, PLACE1001114, PLACE1001123, PLACE1001229, PLACE1001340, PLACE1001407, PLACE1001464, PLACE1001788, PLACE1001795, PLACE1001918, PLACE1002080, PLACE1002095, PLACE1002329, PLACE1002374, PLACE1002518, PLACE1002547, PLACE1002726, PLACE1002905, PLACE1002911, PLACE1002967, PLACE1003163, PLACE1003407, PLACE1003460, PLACE1003573, PLACE1003598, PLACE1003644, PLACE1003772, PLACE1003839, PLACE1003845, PLACE1004078, PLACE1004166, PLACE1004168, PLACE1004199, PLACE1004279, PLACE1004282, PLACE1004441, PLACE1004482, PLACE1004492, PLACE1004637, PLACE1004887, PLACE1005003, PLACE1005005, PLACE1005031, PLACE1005250, PLACE1005410, PLACE1005519, PLACE1005544, PLACE1005660, PLACE1005669, PLACE1005725, PLACE1005736, PLACE1005745, PLACE1005768, PLACE1005815, PLACE1006073, PLACE1006208, PLACE1006219, PLACE1006290, PLACE1006443, PLACE1006809, PLACE1006959, PLACE1007028, PLACE1007296, PLACE1007626, PLACE1007702, PLACE1007845, PLACE1008282, PLACE1008469, PLACE1008657, PLACE1009196, PLACE1009600, PLACE1003735, PLACE1010081, PLACE1010251, PLACE1010713,

PLACE1011116, PLACE1011181,
PLACE1011236, PLACE1011516, PLACE1011708, PLACE1011824, PLACE1011978, PLACE2000118,
PLACE3000181, SKNMC1000004, SKNMC1000014, THYRO1000584, THYRO1000866, THYRO1001113,
THYRO1001128, THYRO1001205, THYRO1001242, THYRO1001495, THYRO1001523, THYRO1001529,
THYRO1001593, THYRO1001608, THYRO1001702, THYRO1001725, THYRO1001770, THYRO1001803,
Y79AA1000117, Y79AA1000207, Y79AA1000226, Y79AA1000270, Y79AA1000426, Y79AA1000777,
Y79AA1000876, Y79AA1000888, Y79AA1000959, Y79AA1001013, Y79AA1001056, Y79AA1001090,
Y79AA1001264, Y79AA1001272, Y79AA1001328, Y79AA1001427, Y79AA1001430, Y79AA1001530,
Y79AA1001592, Y79AA1001727, Y79AA1001793, Y79AA1001799, Y79AA1001863, Y79AA1002022,
Y79AA1002213, Y79AA1002373, Y79AA1002376, Y79AA1002381.

[0216] Signal ratios of EC_AGE_BSA to EC_BSA and of EC_glycated_BSA to EC_BSA were calculated for each gene. Genes with high signal ratios were selected. In the case of calculating the ratio of signal value of 40 or less to that of more than 40, such signal values were, for convenience, taken as 40 instead of the real values. When the ratio EC_AGE_BSA/EC_BSA is 2 or more, expression of the genes exhibiting such ratio is expected to be elevated due to advanced glycation endproduct of bovine serum albumin. The higher the value is, the higher the gene expression level is. When the ratio EC_AGE_BSA/EC_BSA ranges from 0.5 to 2, expression of the genes exhibiting such ratio is expected to be unaffected due to advanced glycation endproduct of bovine serum albumin. When the ratio EC_AGE_BSA/EC_BSA is less than 0.5, expression of the genes exhibiting such ratio value is expected to be decreased due to advanced glycation endproduct of bovine serum albumin. The lower the value is, the lower the gene expression level is.

[0217] Clone with EC_AGE_BSA/BC_BSA ratio of 2 or higher are as follows: NT2RP2001538, NT2RP4001001 and Y79AA1000967.

[0218] These cDNAs are associated with diabetes.

Analysis of genes associated with neural cell differentiation

[0219] Genes involved in neural cell differentiation are useful for treating neurological diseases. It is possible that genes with varying expression levels in response to induction of cellular differentiation in neural cells are associated with neurological diseases.

[0220] A survey was performed for genes of which expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA)) in cultured cells of a neural strain, NT2.

[0221] The NT2 cells were treated basically according to supplier's instruction manual. "Undifferentiated NT2 cells" means NT2 cells successively cultured in an Opti-MEM I (GIBCO-BRL; catalog No. 31985) containing 10%(v/v) fetal bovine serum and 1%(v/v) penicillin-streptomycin (GIBCO BRL). "NT2 cells cultured in the presence of retinoic acid" means the cells resulted from transferring undifferentiated NT2 cells into a retinoic acid-containing medium, which consists of D-MEM (GIBCO BRL; catalog No. 11965), 10%(v/v) fetal bovine serum, 1%(v/v) penicillin-streptomycin and 10.M retinoic acid (GIBCO-BRL), and the subsequent successive culture therein for 5 weeks. "NT2 cells that were cultured in the presence of retinoic acid and then further cultured in the presence of cell-division inhibitor added" means NT2 cells resulted from transferring NT2 cells cultured in the presence of retinoic acid for 5 weeks into a cell-division inhibitor-containing medium, which consisted of D-MEM(GIBCO BRL; catalog No.11965), 10%(v/v) fetal bovine serum, 1%(v/v) penicillin-streptomycin, 10. M retinoic acid, 10.M FudR (5-fluoro-2'-deoxyuridine: GIBCO BRL), 10. M Urd (Uridine: GIBCO BRL) and 1.M araC (Cytosine.-D-Arabinofuranoside: GIBCO BRL), and the subsequence successive culture for 2 weeks. Each of the cells were treated with trypsin and then harvested. Total RNAs were extracted from the cells by using S.N.A.P.(TM) Total RNA Isolation kit (Invitrogen). The labeling of probe used for hybridization was carried out by using 10.g of the total RNA according to the same methods as described above. The data were obtained in triplicate (n=3). The data of signal value representing gene expression level in the cells in the presence of stimulation for inducing differentiation were compared with those in the absence of the stimulation. The comparison was performed by statistical treatment of two-sample t-test. Clones with significant difference in the signal distribution were selected under the condition of $p<0.05$. In this analysis, clones with the difference can be statistically detected even when the signals were low. Accordingly, clones with signal value of 40 or less were also assessed for the selection.

[0222] Tables 186-365 show the expression level of each cDNA in undifferentiated NT2 cells, NT2 cells cultured in the presence of RA, and NT2 cells that were cultured in the presence of RA and that were further cultured in the presence of cell-division inhibitor added.

[0223] Averaged signal values (M_1, M_2) and sample variances (s_1^2, s_2^2) were calculated for each gene in each of the cells, and then, the pooled sample variances s^2 were obtained from the sample variances of the two types of cells to be compared. The t values were determined according to the following formula: $t=(M1-M2)/s/(1/3+1/3)^{1/2}$. When the determined t-value was greater than a t-value at P, which means the probability of significance level, of 0.05 or 0.01 in the t-distribution table with 4 degrees of freedom, the difference was judged to be found in the expression level of the gene between the two types of cells at $p<0.05$ or $p<0.01$, respectively. The tables also include the information on

an increase (+) or decrease (-) in the expression level of a gene in the treated cells when the level is compared with that of untreated undifferentiated cells.

[0224] Clones of which expression levels increased by RA are as follows: HEMBA1000121, HEMBA1000275, HEMBA1000300, HEMBA1000634, HEMBA1000671, HEMBA1000875, HEMBA1001184, HEMBA1001390, HEMBA1001886, HEMBA1002163, HEMBA1002227, HEMBA1002420, HEMBA1002421, HEMBA1003072, HEMBA1003120, HEMBA1003294, HEMBA1003497, HEMBA1004007, HEMBA1004110, HEMBA1004391, HEMBA1004444, HEMBA1005230, HEMBA1005246, HEMBA1005267, HEMBA1005489, HEMBA1005913, HEMBA1006299, HEMBA1006357, HEMBA1006517, HEMBA1006544, HEMBA1006658, HEMBA1006749, HEMBA1007063, HEMBA1007241, HEMBB1000447, HEMBB1000542, HEMBB1000567, HEMBB1000642, HEMBB1000668, HEMBB1001026, HEMBB1001847, HEMBB1002051, HEMBB1002120, HEMBB1002228, HEMBB1002693, MAMMA1000106, MAMMA1000141, MAMMA1000473, MAMMA1000528, MAMMA1000810, MAMMA1000881, MAMMA1001634, MAMMA1001957, MAMMA1002205, MAMMA1002224, NT2RM2000423, NT2RM2000497, NT2RM2000582, NT2RM2001126, NT2RM2001902, NT2RM4000198, NT2RM4000284, NT2RM4000593, NT2RM4001321, NT2RP1000002, NT2RP1000050, NT2RP1000181, NT2RP1000261, NT2RP1000465, NT2RP1000468, NT2RP1000579, NT2RP1000679, NT2RP2000092, NT2RP2000479, NT2RP2000610, NT2RP2000663, NT2RP2000694, NT2RP2000903, NT2RP2001388, NT2RP2001538, NT2RP2001878, NT2RP2001015, NT2RP2002304, NT2RP2002721, NT2RP2002824, NT2RP2002942, NT2RP2002974, NT2RP2002976, NT2RP2003179, NT2RP2003302, NT2RP2003383, NT2RP2003469, NT2RP2003664, NT2RP2003940, NT2RP2004069, NT2RP2004108, NT2RP2004524, NT2RP2004556, NT2RP2004670, NT2RP2005069, NT2RP2005247, NT2RP2005425, NT2RP2005463, NT2RP2005514, NT2RP2005535, NT2RP2005541, NT2RP2005774, NT2RP2005878, NT2RP2005883, NT2RP2005887, NT2RP2006099, NT2RP2006134, NT2RP3000011, NT2RP3000125, NT2RP3000171, NT2RP3000232, NT2RP3000460, NT2RP3000481, NT2RP3000652, NT2RP3000677, NT2RP3000818, NT2RP3000820, NT2RP3001044, NT2RP3001061, NT2RP3001170, NT2RP3001240, NT2RP3001322, NT2RP3001388, NT2RP3001542, NT2RP3001592, NT2RP3001976, NT2RP3002790, NT2RP3002900, NT2RP3002983, NT2RP3003000, NT2RP3003354, NT2RP3003532, NT2RP3003729, NT2RP3003874, NT2RP3003939, NT2RP3004025, NT2RP3004083, NT2RP3004090, NT2RP3004130, NT2RP3004202, NT2RP3004294, NT2RP3004640, NT2RP4000108, NT2RP4000634, NT2RP4002451, NT2RP4002715, OVARC1000090, OVARC1000208, OVARC1000275, OVARC1000553, OVARC1000775, OVARC1000853, OVARC1000873, OVARC1000916, OVARC1000995, OVARC1001030, OVARC1001049, OVARC1001132, OVARC1001596, OVARC1002178, PLACE1000258, PLACE1000442, PLACE1000927, FLACE1000986, PLACE1001100, PLACE1001123, PLACE1001795, PLACE1002518, PLACE1002547, PLACE1002967, PLACE1003407, PLACE1003428, PLACE1003644, PLACE1003839, PLACE1004078, PLACE1004441, PLACE1004450, PLACE1005669, PLACE1005682, PLACE1005736, PLACE1005768, PLACE1005815, PLACE1006073, PLACE1006208, PLACE1007296, PLACE1007626, PLACE1008282, PLACE1008984, PLACE1008985, PLACE1010445, PLACE1011708, PLACE1011978, PLACE4000455, SKNMC1000004, THYRO1000036, THYRO1000580, THYRO1000776, THYRO1000999, THYRO1001063, THYRO1001128, THYRO1001205, THYRO1001327, THYRO1001523, THYRO1001725, THYRO1001770, Y79AA1000207, Y79AA1000226, Y79AA1000270, Y79AA1001056, Y79AA1001062, Y79AA1001090, Y79AA1001727, Y79AA1002213, Y79AA1002381.

[0225] Clones of which expression levels decreased by RA are as follows: BNGH41000020, HEMBA1005070, NT2RP2005027, NT2RP3003473, Y79AA1002376.

[0226] Clones of which expression levels increase by RA/inhibitor are as follows: HEMBA1000128, HEMBA1000875, HEMBA1001390, HEMBA1002163, HEMBA1002227, HEMBA1002421, HEMBA1004391, HEMBA1004454, HEMBA1004785, HEMBA1005913, HEMBA1006171, HEMBA1006299, HEMBA1006335, HEMBA1006544, HEMBA1007241, HEMBB1000447, HEMBB1000668, MAMMA1000994, MAMMA1001344, NT2RM2000582, NT2RP1001004, NT2RP2000663, NT2RP2000694, NT2RP2000903, NT2RP2001388, NT2RP2002674, NT2RP2002974, NT2RP2003383, NT2RP2004069, NT2RP2004606, NT2RP2004837, NT2RP2005069, NT2RP2005425, NT2RP2005463, NT2RP2005541, NT2RP2005883, NT2RP2005887, NT2RP3000460, NT2RP3000838, NT2RP3001044, NT2RP3001240, NT2RP3001388, NT2RP3002721, NT2RP3002738, NT2RP3003469, NT2RP3004083, NT2RP3004130, NT2RP3004202, NT2RP3004294, NT2RP3004640, NT2RP4000108, NT2RP4002451, NT2RP4002715, OVARC1000275, OVARC1000467, OVARC1000553, OVARC1000853, OVARC1000873, OVARC1000916, OVARC1000995, OVARC1001030, OVARC1001222, OVARC1001596, OVARC1002058, OVARC1002178, PLACE1000927, PLACE1001123, PLACE1001407, PLACE1001464, PLACE1001564, PLACE1001795, PLACE1002547, PLACE1003407, PLACE1003644, PLACE1003845, PLACE1004441, PLACE1004482, PLACE1005410, PLACE1005601, PLACE1005725, PLACE1005736, PLACE1006093, PLACE1006219, PLACE1006290, PLACE1006716, PLACE1007296, PLACE1007626, PLACE1008359, PLACE1010968, PLACE1011364,

PLACE1011824, THYRO1000678, THYRO1000776, THYRO1000999, THYRO1001113, THYRO1001237, THYRO1001523, Y79AA1000226, Y79AA1000888, Y79AA1001430.

[0227] Clones of which expression levels decrease by RA/inhibitor are as follows: HEMBA1000349, HEMBA1001297, HEMBA1001878, HEMBA1005070, HEMBA1006482, HEMBB1001959, NT2RM2001939, NT2RP1000981, NT2RP2001469, NT2RP3003473, OVARC1001132, PLACE1001655, Y79AA1000127, Y79AA1002381.

[0228] Clones of which expression levels increase in the presence of both RA and RA/inhibitor are as follows: HEMBA1000875, HEMBA1001390, HEMBA1002163, HEMBA1002227, HEMBA1002421, HEMBA1004391, HEMBA1005913, HEMBA1006299, HEMBA1006544, HEMBA1007241, HEMBB1000447, HEMBB1000668, NT2RM2000582, NT2RP2000663, NT2RP2000694, NT2RP2000903, NT2RP2001388, NT2RP2002974, NT2RP2003383, NT2RP2004069, NT2RP2005069, NT2RP2005425, NT2RP2005463, NT2RP2005541, NT2RP2005883, NT2RP2005887, NT2RP3000460, NT2RP3001044, NT2RP3001240, NT2RP3001388, N12RP3004083, NT2RP3004130, NT2RP3004202, NT2RP3004294, NT2RP3004640, NT2RP4000108, NT2RP4002451, NT2RP4002715, OVARC1000275, OVARC1000553, OVARC1000853, OVARC1000873, OVARC1000916, OVARC1000995, OVARC1001030, OVARC1001596, OVARC1002178, PLACE1000927, PLACE1001123, PLACE1001795, PLACE1002547, PLACE1003407, PLACE1003644, PLACE1004441, PLACE1005736, PLACE1007296, PLACE1007626, THYRO1000776, THYRO1000999, THYRO1001523, Y79AA1000226.

[0229] Clones of which expression levels decrease in the presence of both RA and RA/inhibitor are as follows: HEMBA1005070 and NT2RP3003473.

[0230] These are neurological disease-associated clones.

Analysis of rheumatoid arthritis-associated genes

[0231] The onset of rheumatoid arthritis is thought to be involved in the proliferation of synovial cells covering inner surfaces of joint cavity and in inflammatory reaction resulted from the action of cytokines produced by leukocytes infiltrating into the joint synovial tissues (Rheumatism Information Center.http://www.rheuma-net.or.jp/). Recent studies have also revealed that tissue necrosis factor (TNF)-. participates in the onset (Current opinion in immunology 1999, 11, 657-662). When the expression of a gene exhibits responsiveness to the action of TNF on synovial cells, the gene is considered to be involved in rheumatoid arthritis.

[0232] A survey was performed for genes of which expression levels are varied in response to TNF-. in the primary cell culture of synovial tissue. The primary cultured cells of the smooth muscle (Cell Applications) were grown to be confluent in a culture dish, and then, human TNF-. (Boehringer-Mannheim) was added at a final concentration of 10 ng/ml thereto. The culture was further continued for 24 hours.

[0233] Total RNA was extracted from the cells by using S.N.A.P.(TM) Total RNA Isolation kit (Invitrogen). The labeling of probe used for hybridization was carried out by using 10.g of the total RNA according to the same methods as described above. The data were obtained in tripricate (n=3). The data of signal value representing gene expression level in the cells in the presence of TNF stimulation were compared with those in the absence of the stimulation. The comparison was performed by statistical treatment of two-sample t-test. Clones with significant difference in the signal distribution were selected under the condition of $p<0.05$. In this analysis, clones with the difference can be statistically detected even when the signals were low. Accordingly, clones with signal value of 40 or less were also assessed for the selection.

[0234] Table 366 shows the expression level of each cDNA in synovial cells cultured in the absence or presence of TNF.

[0235] Averaged signal values (M_1, M_2) and sample variances (s_1^2, s_2^2) for each gene were calculated in each of the cells, and then, the pooled sample variances s^2 were obtained from the sample variances of the two types of cells to be compared. The t-values were determined according to the following formula: $t=(M_1-M_2)/s/(1/3+1/3)^{1/2}$. When the determined t-value was greater than a t-value at P, which means the probability of significance level, of 0.05 or 0.01 in the t-distribution table with 4 degrees of freedom, the difference was judged to be found in the expression level of the gene between the two types of cells at $p<0.05$ or $p<0.01$, respectively. The tables also include the information of an increase (+) or decrease (-) in the expression level of a gene in the stimulated cells when the level is compared with that of unstimulated cells.

[0236] Clones of which expression levels are elevated by TNF-. are as follows: BNGH41000020, HEMBA1000349, HEMBA1000634, HEMBA1000671, HEMBA1000835, HEMBA1000962, HEMBA1002178, HEMBA1002195, HEMBA1002239, HEMBA1002420, HEMBA1002524, HEMBA1002992, HEMBA1003315, HEMBA1003392, HEMBA1003487, HEMBA1003602, HEMBA1004067, HEMBA1004797, HEMBA1005337, HEMBA1005489, HEMBA1006916, HEMBB1000668, HEMBB1000905, HEMBB1001547, HEMBB1001573, HEMBB1002041, HEMBB1002663, MAMMA1000652, MAMMA1000810, MAMMA1001634,

MAMMA1002091, MAMMA1002234, NT2RM2000306, NT2RM4000417, NT2RP1000002, NT2RP1000181, NT2RP1000740, NT2RP2000694, NT2RP2001921, NT2RP2002527, NT2RP2004495, NT2RP2004606, NT2RP2005163, NT2RP2005463, NT2RP2006134, NT2RP3000171, NT2RP3000652, NT2RP3001195, NT2RP3001976, NT2RP3003473, NT2RP3003874, NT2RP3004090, NT2RP3004294, NT2RP3004557, NT2RP3004647, NT2RP4000108, NT2RP4001001, NT2RP4001877, OVARC1000090, OVARC1000105, OVARC1000275, OVARC1000439, OVARC1001607, PLACE1000740, PLACE1000927, PLACE1001016, PLACE1001100, PLACE1001464, PLACE1001500, PLACE1001918, PLACE1002095, PLACE1002547, PLACE1003644, PLACE1004519, PLACE1005031, PLACE1005410, PLACE1005736, PLACE1006219, PLACE1006809, PLACE1008716, PLACE1010081, THYRO1001770, Y79AA1000127, Y79AA1000207, Y79AA1000270, Y79AA1000876, Y79AA1001013, Y79AA1001264, Y79AA1001272, Y79AA1001328, Y79AA1001430, Y79AA1001530, Y79AA1001799.

[0237] Clones of which expression levels decrease by TNF-. are as follows: NT2RM4000326, NT2RP1000300, NT2RP2000514, NT2RP2001755, NT2RP2006042, NT2RP3000481, NT2RP3002790. These are rheumatoid arthritis-associated clones.

EXAMPLE 16

Search for a signal sequence, transmembrane region and functional domain in deduced amino acid sequences

[0238] The deduced amino acid sequences from the full-length nucleotide sequences were examined to predict the presence of a signal sequence in their amino-termini as well as the presence of a transmembrane region. The amino acid sequences were also searched for a protein functional domain (motif). The examinations for a signal sequence in the amino-terminus, for a transmembrane region and for a functional domain were performed by using PSORT [K. Nakai & M. Kanehisa, Genomics, 14:897-911 (1992)], SOSUI [T. Hirokawa et al., Bioinformatics, 14:378-379 (1998)] (Mitsui Knowledge Industry Co., Ltd.) and Pfam (http://www.sanger.ac.uk/Software/Pfam/index.shtml), respectively. When the presence of a signal sequence or a transmembrane region in the amino-terminus was predicted in the amino acid sequence by PSORT or SOSUI, the protein was predicted to be a secretory protein or a transmembrane protein. When the amino acid sequence matched a functional domain in the Pfam search for a functional domain, the function of the protein is predictable based on the matching data, for example, by referring to the functional categories in PROSITE (http://www.expasy.ch/cgi-bin/prosite-list.pl). The functional domain search can be performed by using PROSITE instead of Pfam.

[0239] Search results obtained by using the respective software programs are indicated below.

[0240] Clones whose deduced amino acid sequences were predicted to have signal sequences by PSORT search are as follows:

HEMBA1000713, HEMBA1002420, HEMBA1002421, HEMBA1003101, HEMBA1004110, HEMBA1006707, HEMBA1006902, HEMBB1001530, HEMBB1001573, HEMBB1001978, HEMBB1002162, HEMBB1002245, HEMBB1002427, MAMMA1000102, MAMMA1000118, MAMMA1000457, MAMMA1001043, MAMMA1001344, MAMMA1001893, MAMMA1002070, MAMMA1002165, MAMMA1002633, NT2RM2000241, NT2RM2000410, NT2RM2001941, NT2RM4001325, NT2RP1001563, NT2RP2001495, NT2RP2002063, NT2RP2002721, NT2RP2003383, NT2RP2003593, NT2RP2003655, NT2RP2003664, NT2RP2004179, NT2RP2004205, NT2RP2004524, NT2RP2005463, NT2RP3000460, NT2RP3001012, NT2RP3001858, NT2RP3002836, NT2RP3003076, NT2RP3003532, NT2RP3004133, NT2RP3004309, NT2RP4001467, NT2RP4002451, OVARC1000298, OVARC1000811, PLACE1000231, PLACE1000740, PLACE1001183, PLACE1001536, PLACE1001564, PLACE1002095, PLACE1002374, PLACE1003839, PLACE1001482, PLACE1005005, PLACE1005250, PLACE1005383, PLACE1005410, PLACE1005544, PLACE1005569, PLACE1006093, PLACE1006277, PLACE1006809, PLACE1007626, PLACE1008359, PLACE1009067, PLACE1010251, PLACE1011236, SKNMC1000004, SKNMC1000014, THYRO1000099, THYRO1000196, THYRO1001237, THYRO1001327, THYRO1001523, THYRO1001702, THYRO1001725, Y79AA1000426, Y79AA1000521, Y79AA1000959, Y79AA1001013, Y79AA1001264, Y79AA1001328, Y79AA1001427, Y79AA1001430, Y79AA1001795, Y79AA1001803, Y79AA1002022,

[0241] Clones whose deduced amino acid sequences were predicted to have transmembrane regions by SOSUI search are as follows: BNGH41000091, HEMBA1000121, HEMBA1000349, HEMBA1000477, HEMBA1000713, HEMBA1000940, HEMBA1000962, HEMBA1001221, HEMBA1001228, HEMBA1001621, HEMBA1002167, HEMBA1002195, HEMBA1002227, HEMBA1002421, HEMBA1003101, HEMBA1003392, HEMBA1003530, HEMBA1003732, HEMBA1003945, HEMBA1004391, HEMBA1004454, HEMBA1004797, HEMBA1004982, HEMBA1005449, HEMBA1005522, HEMBA1005545, HEMBA1005698, HEMBA1006171, HEMBA1006299, HEMBA1006311, HEMBA1006335, HEMBA1006357, HEMBA1006430, HEMBA1006724, HEMBA1006960, HEMBB1000407, HEMBB1000447, HEMBB1000567, HEMBB1000679, HEMBB1000905, HEMBB1001026,

HEMBB1001407, HEMBB1001573, HEMBB1001978, HEMBB1002041, HEMBB1002162, HEMBB1002245, HEMBB1002427, HEMBB1002693, MAMMA1000102, MAMMA1000106, MAMMA1000118, MAMMA1000141, MAMMA1000204, MAMMA1000226, MAMMA1000457, MAMMA1000473, MAMMA1000591, MAMMA1000681, MAMMA1000810, MAMMA1000986, MAMMA1001043, MAMMA1001141, MAMMA1001237, MAMMA1001344, MAMMA1001893, MAMMA1001957, MAMMA1001978, MAMMA1002070, MAMMA1002091, MAMMA1002095, MAMMA1002633, NT2RM1000580, NT2RM1000855, NT2RM1000858, NT2RM2000410, NT2RM2000565, NT2RM2001626, NT2RM2001939, NT2RM2001941, NT2RM4000444, NT2RM4000587, NT2RM4000648, NT2RM4000997, NT2RM4001325, NT2RM4001735, NT2RM4001768, NT2RM4002352, NT2RP1000050, NT2RP1000181, NT2RP1000261, NT2RP1000300, NT2RP1000448, NT2RP1000551, NT2RP1000613, NT2RP1000981, NT2RP1001563, NT2RP2000479, NT2RP2000533, NT2RP2000649, NT2RP2000663, NT2RP2000694, NT2RP2000818, NT2RP2000903, NT2RP2001200, NT2RP2001276, NT2RP2001495, NT2RP2001915, NT2RP2001956, NT2RP2002188, NT2RP2002232, NT2RP2002527, NT2RP2002533, NT2RP2002721, NT2RP2002824, NT2RP2002942, NT2RP2002976, NT2RP2003042, NT2RP2003390, NT2RP2003469, NT2RP2003593, NT2RP2003655, NT2RP2003664, NT2RP2003950, NT2RP2004179, NT2RP2004205, NT2RP2004495, NT2RP2004524, NT2RP2004556, NT2RP2004606, NT2RP2004648, NT2RP2004794, NT2RP2005163, NT2RP2005181, NT2RP2005463, NT2RP2005597, NT2RP2005666, NT2RP2005883, NT2RP2005994, NT2RP2006004, NT2RP2006269, NT2RP2006512, NT2RP2006580, NT2RP3000169, NT2RP3000171, NT2RP3000304, NT2RP3000460, NT2RP3000616, NT2RP3000721, NT2RP3000818, NT2RP3000907, NT2RP3000921, NT2RP3001159, NT2RP3001195, NT2RP3001240, NT2RP3001271, NT2RP3001322, NT2RP3001388, NT2RP3001560, NT2RP3001592, NT2RP3001650, NT2RP3001738, NT2RP3002015, NT2RP3002311, NT2RP3002342, NT2RP3002411, NT2RP3002790, NT2RP3002836, NT2RP3002900, NT2RP3002958, NT2RP3003000, NT2RP3003354, NT2FP3003532, NT2RP3003535, NT2RP3003614, NT2RP3004025, NT2RP3004075, NT2RP3004083, NT2RP3004090, NT2RP3004130, NT2RP3004294, NT2RP3004309, NT2RP3004345, NT2RP3004406, NT2RP3004481, NT2RP3004552, NT2RP4001001, NT2RP4001009, NT2RP4001467, NT2RP4001879, NT2RP4002187, NT2RP4002451, NT2RP4002750, OVARC1000003, OVARC1000105, OVARC1000307, OVARC1000439, OVARC1000553, OVARC1001030, OVARC1001336, OVARC1001570, PLACE1000231, PLACE1000560, PLACE1000740, PLACE1000912, PLACE1000914, PLACE1000927, PLACE1001016, PLACE1001183, PLACE1001231, PLACE1001401, PLACE1001407, PLACE1001464, PLACE1001536, PLACE1001564, PLACE1001655, PLACE1001836, PLACE1001918, PLACE1001949, PLACE1002518, PLACE1002726, PLACE1002967, PLACE1003573, PLACE1003737, PLACE1003839, PLACE1003845, PLACE1003852, PLACE1004279, PLACE1004282, PLACE1004441, PLACE1004637, PLACE1004648, PLACE1004816, PLACE1004887, PLACE1005003, PLACE1005005, PLACE1005410, PLACE1005544, PLACE1005569, PLACE1005660, PLACE1005725, PLACE1005745, PLACE1005927, PLACE1006290, PLACE1006443, PLACE1006959, PLACE1007096, PLACE1007296, PLACE1007626, PLACE1007881, PLACE1008359, PLACE1008469, PLACE1008716, PLACE1008985, PLACE1009196, PLACE1009279, PLACE1009527, PLACE1009546, PLACE1009600, PLACE1010011, PLACE1010078, PLACE1010445, PLACE1010713, PLACE1010784, PLACE1010968, PLACE1011236, PLACE1011516, PLACE3000181, THYRO1000400, THYRO1000678, THYRO1000776, THYRO1000956, THYRO1001102, THYRO1001113, THYRO1001205, THYRO1001237, THYRO1001242, THYRO1001266, THYRO1001327, THYRO1001478, THYRO1001523, THYRO1001641, THYRO1001702, THYRO1001725, Y79AA1000207, Y79AA1000226, Y79AA1000270, Y79AA1000521, Y79AA1000888, Y79AA1001013, Y79AA1001212, Y79AA1001264, Y79AA1001328, Y79AA1001426, Y79AA1001427, Y79AA1001727, Y79AA1001787, Y79AA1001795, Y79AA1001803, Y79AA1002058, Y79AA1002129, Y79AA1002213, Y79AA1002373,

[0242] Names of clones whose deduced amino acid sequences were predicted to have functional domains by Pfam search, and names of the matched functional domains are shown below. When multiple functional domains matched a clone, each domain name was indicated, separated by a double-slash mark,//.

HEMBA1000006//Src homology domain 3
HEMBA1000128//SCP-like extracellular Proteins
HEMBA1000349//ABC transporters
HEMBA1000462//RNA recognition motif. (aka RRM, RBD, or RNP domain)
HEMBA1000590//EGF-like domain//von Willebrand factor type A domain
HEMBA1000671//Zinc finger, C2H2 type
HEMBA1000732//EGF-like domain
HEMBA1000940//Connexin
HEMBA1001221//EGF-like domain//Kazal-type serine protease inhibitor domain

HEMBA1001621//7 transmembrane receptor (rhodopsin family)
HEMBA1001878//WD domain, G-beta repeats
HEMBA1002048//Zinc finger, C2H2 type
HEMBA1002167//Carboxylesterases
HEMBA1002551//WD domain, G-beta repeats
HEMBA1002992//Ubiquitin family
HEMBA1003047//CUB domain
HEMBA1003120//Zinc finger, C2H2 type
HEMBA1003230//EGF-like domain
HEMBA1003392//Low-density lipoprotein receptor domain class A
HEMBA1003497//Zinc finger, C2H2 type
HEMBA1004250//Cadherin
HEMBA1004391//Fibronectin type III domain//IG superfamily
HEMBA1004454//4 transmembrane segments integral membrane proteins
HEMBA1004785!/'chromo' (CHRromatin Organization MOdifier) domain
HEMBA1005246//Zinc finger, C2H2 type
HEMBA1005267//Ank repeat
HEMBA1005545//7 transmembrane receptor (rhodopsin family)
HEMBA1005929//Eukaryotic protein kinase domain
HEMBA1005945//Mitochondrial carrier proteins
HEMBA1006572//Zinc finger, C2H2 type
HEMBA1006707//EGF-like domain//von Willebrand factor type A domain
HEMBA1006749//EGF-like domain//von Willebrand factor type A domain
HEMBA1006770//RNA recognition motif. (aka RRM, RBD, or RNP domain)
HEMBA1006902//EGF-like domain//von Willebrand factor type A domain
HEMBB1000106//Zinc finger, CCHC class
HEMBB1000668//WD domain, G-beta repeats
HEMBB1000881//Thrombospondin type 1 domain
HEMBB1000905//WD domain, G-beta repeats
HEMBB1002041//EGF-like domain//Kazal-type serine protease inhibitor domain
HEMBB1002245//IG superfamily
HEMBB1002302//Zinc finger, CCHC class
HEMBB1002465//Acyl-CoA dehydrogenases
HEMBB1002661//Helix-loop-helix DNA-binding domain
MAMMA1000204//C2 domain
MAMMA1000457//FAD/NAD-binding domain in oxidoreductases
MAMMA1000681//7 transmembrane receptor (rhodopsin family)
MAMMA1000881//Eukaryotic protein kinase domain//Protein kinase C terminal domain
MAMMA1001150//Phorbol esters / diacylglycerol binding domain//Eukaryotic protein kinase domain
MAMMA1001310//WD domain, G-beta repeats
MAMMA1001532//Zinc finger, C2H2 type
MAMMA1001615//Helix-loop-helix DNA-binding domain
MAMMA1002070//Kringle domain
MAMMA1002080//Ras family (contains ATP/GTP binding P-loop)
MAMMA1002095//E1-E2 ATPases
MAMMA1002165//Insulin-like growth factor binding proteins
NT2RM1000789//HMG (high mobility group) box
NT2RM1000855//eubacterial secY protein
NT2RM1000899//Mitochondrial carrier proteins
NT2RM2000589//PH (pleckstrin homology) domain
NT2RM2000632//Helicases conserved C-terminal domain
NT2RM2001792//Fibrinogen beta and gamma chains, C-terminal globular domain
NT2RM2001902//Eukaryotic protein kinase domain
NT2RM2001939//7 transmembrane receptor (rhodopsin family)
NT2RM2001941//7 transmembrane receptor (rhodopsin family)
NT2RM4000284//Class I Histocompatibility antigen, domains alpha 1 and 2
NT2RM4000326//Zinc finger, C2H2 type
NT2RM4000417//C2 domain

NT2RM4000444//ABC transporters
NT2RM4001377//PH (pleckstrin homology) domain
NT2RM4001768//Alcohol/other dehydrogenases, short chain type
NT2RM4002352//Low-density lipoprotein receptor domain class A
NT2RP1000181//Heme-binding domain in cytochrome b5 and oxidoreductases
NT2RP1000271//Zinc finger, C2H2 type
NT2RP1000325//Mitochondrial carrier proteins
NT2RP1000613//Eukaryotic-type carbonic anhydrases
NT2RP1000981//IG superfamily
NT2RP1001004//Thrombospondin type 1 domain
NT2RP1001020//Eukaryotic protein kinase domain
NT2RP1001031//WD domain, G-beta repeats
NT2RP1001563//EGF-like domain//Lectin C-type domain short and long forms//SCP-like extracellular Proteins
NT2RP2000092//Zinc finger, C2H2 type
NT2RP2000514//Fibronectin type III domain//IG superfamily
NT2RP2000649//Zinc-binding metalloprotease domain
NT2RP2000712//Zinc finger, C2H2 type
NT2RP2000739//Zinc finger, C2H2 type
NT2RP2001514//E1-E2 ATPases
NT2RP2001529//Eukaryotic protein kinase domain
NT2RP2001755//Thrombospondin type 1 domain
NT2RP2001769//Eukaryotic protein kinase domain
NT2RP2002188//Carboxylesterases
NT2RP2002527//Heme-binding domain in cytochrome b5 and oxidoreductases
NT2RP2002564//Zinc finger, C2H2 type
NT2RP2002942//IG superfamily
NT2RP2003179//Eukaryotic protein kinase domain
NT2RP2003302//Zinc finger, C2H2 type
NT2RP2003390//DnaJ, prokaryotic heat shock protein
NT2RP2003469//Sugar (and other) transporters
NT2RP2003545//Eukaryotic protein kinase domain
NT2RP2003593//Thioredoxins
NT2RP2003940//Zinc finger, C2H2 type
NT2RP2004108//Zinc finger, C2H2 type
NT2RP2004205//IG superfamily
NT2RP2004670//Eukaryotic protein kinase domain
NT2RP2004847//Zinc finger, C2H2 type
NT2RP2005181//Amino acid permeases
NT2RP2005247//Zinc finger, C3HC4 type (RING finger)
NT2RP2005391//Fibronectin type III domain
NT2RP2005535//Zinc finger, C2H2 type
NT2RP2005774//Zinc finger, C2H2 type
NT2RP2005878//Alcohol/other dehydrogenases, short chain type
NT2RP2005941//Homeobox domain//'Paired box' domain
NT2RP2006004//Fibronectin type III domain
NT2RP3000011//WD domain, G-beta repeats
NT2RP3000022//Eukaryotic protein kinase domain
NT2RP3000063//Zinc finger, C2H2 type
NT2RP3000148//Zinc finger, C2H2 type
NT2RP3000172//Eukaryotic protein kinase domain
NT2RP3000201//Eukaryotic protein kinase domain
NT2RP3000232//Zinc finger, C2H2 type
NT2RP3000304//Low-density lipoprotein receptor domain class A//Low-density lipoprotein receptor domain class B
NT2RP3000436//Thioredoxins
NT2RP3000460//eubacterial secY protein
NT2RP3000616//Fibronectin type III domain
NT2RP3000652//Zinc finger, C2H2 type

NT2RP3000676//Mitochondrial carrier proteins
NT2RP3000789//KH domain family of RNA binding proteins
NT2RP3000820//WD domain, G-beta repeats
NT2RP3000838//PH (pleckstrin homology) domain
NT2RP3000907//E1-E2 ATPases
NT2RP3000921//IG superfamily
NT2RP3001195//Sugar (and other) transporters
NT2RP3001240//eubacterial secY protein
NT2RP3001388//C2 domain
NT2RP3001650//CUB domain//Low-density lipoprotein receptor domain class A
NT2RP3001738//Heme-binding domain in cytochrome b5 and oxidoreductases
NT2RP3001976//Zinc finger, C2H2 type
NT2RP3002281//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RP3002411//Alcohol/other dehydrogenases, short chain type
NT2RP3002721//Citrate synthase
NT2RP3003000//Ion transport proteins
NT2RP3003527//Eukaryotic protein kinase domain
NT2RP3003535//TPR Domain
NT2RP3003849//C2 domain
NT2RP3004067//Src homology domain 3
NT2RP3004090//Zinc finger, C3HC4 type (RING finger)
NT2RP3004481//IG superfamily
NT2RP3004552//CUB domain//Sushi domain
NT2RP3004647//Mitochondrial carrier proteins
NT2RP4000108//Intermediate filament proteins
NT2RP4000634//Eukaryotic protein kinase domain
NT2RP4000962//Eukaryotic protein kinase domain
NT2RP4001009//Zinc-binding metalloprotease domain
NT2RP4001877//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RP4002187//Alcohol/other dehydrogenases, short chain type
NT2RP4002750//Amino acid permeases
OVARC1000105//Ubiquitin-conjugating enzymes
OVARC1000255//Eukaryotic protein kinase domain
OVARC1000313//Thioredoxins
OVARC1000410//Fibrinogen beta and gamma chains, C-terminal globular domain
OVARC1000529//Eukaryotic protein kinase domain
OVARC1000811//CUB domain//Kringle domain
OVARC1000916//Eukaryotic protein kinase domain
OVARC1001049//Helix-loop-helix DNA-binding domain
OVARC1001338//Eukaryotic protein kinase domain
OVARC1001569//Eukaryotic protein kinase domain
OVARC1001570//Eukaryotic aspartyl proteases
PLACE1000231//WAP-type (Whey Acidic Protein) 'four-disulfide core'
PLACE1000258//Zinc finger, C2H2 type
PLACE1000740//EGF-like domain
PLACE1000907//Zinc finger, C2H2 type
PLACE1001016//Ion transport proteins
PLACE1001500//Helicases conserved C-terminal domain
PLACE1001655//Ion transport proteins
PLACE1001795//SCP-like extracellular Proteins
PLACE1001949//E1-E2 ATPases
PLACE1002329//Src homology domain 3
PLACE1002355//Alpha-2-macroglobulin family//Kazal-type serine protease inhibitor domain
PLACE1002374//Cysteine proteases
PLACE1002518//Zinc finger, C3HC4 type (RING finger)
PLACE1002911//IG superfamily
PLACE1003135//Eukaryotic protein kinase domain
PLACE1003163//Enoyl-CoA hydratase/isomerase

PLACE1003573//Lectin C-type domain short and long forms
PLACE1004166//Bromodomain
PLACE1004305//Ras family (contains ATP/GTP binding P-loop)
PLACE1004441//7 transmembrane receptor (rhodopsin family)
PLACE1004520//IG superfamily
PLACE1004816//Fibrinogen beta and gamma chains, C-terminal globular domain
PLACE1004887//Zinc finger, C3HC4 type (RING finger)
PLACE1005003//Trypsin
PLACE1005383//EGF-like domain
PLACE1005410//eubacterial secY protein
PLACE1005426//IG superfamily
PLACE1005519//Eukaryotic protein kinase domain
PLACE1005539//Heat shock hsp20 proteins
PLACE1005544//IG superfamily
PLACE1005569//IG superfamily
PLACE1005682//Zinc finger, C3HC4 type (RING finger)
PLACE1005736//PH (pleckstrin homology) domain
PLACE1006079//Homeobox domain
PLACE1006716//C1q domain
PLACE1008282//Eukaryotic protein kinase domain
PLACE1008549//Ets-domain
PLACE1008744//EGF-like domain//Sushi domain
PLACE1009067//Src homology domain 3
PLACE1010081//Eukaryotic protein kinase domain
PLACE1010251//EGF-like domain
PLACE1010713//Alcohol/other dehydrogenases, short chain type
PLACE1010784//7 transmembrane receptor (rhodopsin family)
PLACE1010968//Fibronectin type III domain
PLACE1011181//ATPases associated with various cellular activities (AAA)
PLACE1011364//Eukaryotic protein kinase domain
PLACE1011407//Zinc finger, C2H2 type
PLACE1011708//CUB domain
PLACE1011824//Eukaryotic protein kinase domain
PLACE1011978//Zinc finger, C2H2 type
PLACE3000181//Cadherin
PLACE3000213//Sushi domain
PLACB4000354//BGF-like domain//Sushi domain
SKNMC1000082//Mitochondrial carrier proteins
THYRO1000196//Cadherin
THYRO1000580//Zinc finger, C2H2 type
THYRO1000678//Connexin
THYRO1000795//Mitochondrial carrier proteins
THYRO1000956//7 transmembrane receptor (rhodopsin family)
THYRO1001113//C2 domain
THYRO1001266//Sodium:solute symporter family
THYRO1001457//Phorbol esters / diacylglycerol binding domain//Bukaryotic protein kinase domain
THYRO1001478//EF hand
THYRO1001593//Eukaryotic protein kinase domain
THYRO1001700//Eukaryotic protein kinase domain
THYRO1001770//Eukaryotic protein kinase domain
Y79AA1000030//WW/rsp5/WWP domain containing proteins
Y79AA1000426//Transforming growth factor beta like domain
Y79AA1000777//WD domain, G-beta repeats
Y79AA1000876//Thioredoxins
Y79AA1000967//Eukaryotic protein kinase domain
Y79AA1001090//Ank repeat
Y79AA1001264//DnaJ, prokaryotic heat shock protein
Y79AA1001328//EGF-like domain

Y79AA1001427//FAD/NAD-binding domain in oxidoreductases
Y79AA1001523//Bromodomain//Zinc finger, C3HC4 type (RING finger)
Y79AA1001530//Tubulin
Y79AA1001727//IG superfamily
Y79AA1001787//E1-E2 ATPases
Y79AA1001799//Mitochondrial carrier proteins
Y79AA1002022//IG superfamily
Y79AA1002381//Eukaryotic protein kinase domain

EXAMPLE 17

Functional categories based on the full-length nucleotide sequences

[0243] Prediction of functions of proteins encoded by the clones and the categorization thereof were performed based on the results of homology search (see homology search result 10) of the databases, GenBank, Swiss-Prot and Uni-Gene for the full-length nucleotide sequences of 826 clones as well as based on the results of domain search (see Example 16) of the deduced amino acid sequences encoded by the full-length nucleotide sequences. (HEMBA1005337, NT2RM1000407, NT2RM2001767, and NT2RP3003939 were excluded because of the absence of full-length sequence.)

[0244] There are 611 clones that presumably encode proteins belonging to any of categories of secretory and/or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins and disease-associated proteins.

[0245] The clones presumably encoding proteins categorized into secretory and/or membrane proteins are those which matched the full-length sequences of Swiss-Prot database with keywords "growth factor", "cytokine", "hormone", "signal", "transmembrane", "membrane", "extracellular matrix", "receptor", "G-protein coupled receptor", "ionic channel", "voltage-gated channel", "calcium channel", "cell adhesion", "collagen" or "connective tissue"; those which matched the data, suggesting that the proteins are secretory and/or membrane proteins; or those which matched the full-length sequences of GenBank or UniGene database with similar description; and, further, those predicted to have an N-terminal signal sequence or a transmembrane region as a result of domain search for the amino acid sequences deduced from the full-length nucleotide sequences.

[0246] The clones presumably encoding proteins categorized into glycoprotein-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "glycoprotein"; those which matched the data, suggesting that the proteins are glycoprotein; or those which matched the full-length sequences of GenBank or UniGene database.

[0247] The clones presumably encoding proteins categorized into signal transduction-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "serine/threonine-protein kinase", "tyrosine-protein kinase" or "SH3 domain"; those which matched the data, suggesting that the proteins are signal transduction-associated proteins (for example, "ADP-ribosylation factor"); or those which matched the the full-length sequences of GenBank or UniGene database with similar description.

[0248] The clones presumably encoding proteins categorized into transcription-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "transcription regulation", "zinc finger" or "homeobox"; those which matched the data, suggesting that the proteins are transcription-associated proteins; or those which matched the full-length sequences of GenBank or UniGene database with similar description.

[0249] The clones presumably encoding proteins categorized into disease-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "disease mutation" or "syndrome"; those which matched the data, suggesting that the proteins are disease-associated proteins; or those which matched the full-length sequences of Swiss-Prot database and GenBank or UniGene database where the matched sequences are those of genes or proteins which had been deposited in the database of Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/Omim/), which is a database of human genes and diseases.

[0250] The following 437 clones were categorized into secretory and/or membrane proteins.

BNGH41000020, BNGH41000087, BNGH41000091, HEMBA1000121, HEMBA1000128, HEMBA1000349, HEMBA1000477, HEMBA1000590, HEMBA1000713, HEMBA1000732, HEMBA1000745, HEMBA1000835, HEMBA1000940, HEMBA1000962, HEM8A1001221, HEMBA1001228, HEMBA1001621, HEMBA1002131, HEMBA1002163, HEMBA1002167, HEMBA1002178, HEMBA1002195, HEMBA1002227, HEMBA1002420, HEMBA1002421, HEMBA1002767, HEMBA1003047, HEMBA1003101, HEMBA1003230, HEMBA1003392, HEMBA1003530, HEMBA1003602, HEMBA1003732, HEMBA1003945, HEMBA1004110, HEMBA1004250, HEMBA1004391, HEMBA1004444, HEMBA1004454, HEMBA1004505, HEMBA1004797, HEMBA1004982, HEMBA1005070, HEMBA1005449, HEMBA1005522, HEMBA1005545, HEMBA1005698, HEMBA1005945,

HEMBA1006171, HEMBA1006299, HEMBA1006311, HEMBA1006335, HEMBA1006357, HEMBA1006430, HEMBA1006482, HEMBA1006707, HEMBA1006724, HEMBA1006749, HEMBA1006902, HEMBA1006960, HEMBA1007241, HEMBB1000407, HEMBB1000447, HEMBB1000567, HEMBB1000679, HEMBB1000881, HEMBB1001026, HEMBB1001048, HEMBB1001407, HEMBB1001530, HEMBB1001573, HEMBB1001847, HEMBB1001978, HEMBB1002041, HEMBB1002162, HEMBB1002245, HEMBB1002427, HEMBB1002693, MAMMA1000102, MAMMA1000106, MAMMA1000118, MAMMA1000141, MAMMA1000204, MAMMA1000226, MAMMA1000457, MAMMA1000473, MAMMA1000496, MAMMA1000591, MAMMA1000681, MAMMA1000810, MAMMA1000986, MAMMA1000994, MAMMA1001043, MAMMA1001141, MAMMA1001237, MAMMA1001344, MAMMA1001418, MAMMA1001893, MAMMA1001957, MAMMA1001978, MAMMA1002070, MAMMA1002091, MAMMA1002095, MAMMA1002165, MAMMA1002234, MAMMA1002586, MAMMA1002633, MAMMA1003126, NT2RM1000462, NT2RM1000542, NT2RM1000580, NT2RM1000855, NT2RM1000858, NT2RM1000899, NT2RM2000241, NT2RM2000410, NT2RM2000423, NT2RM2000565, NT2RM2001626, NT2RM2001792, NT2RM2001939, NT2RM2001941, NT2RM4000198, NT2RM4000284, NT2RM4000417, NT2RM4000444, NT2RM4000587, NT2RM4000593, NT2RM4000648, NT2RM4000761, NT2RM4000997, NT2RM4001325, NT2RM4001735, NT2RM4001768, NT2RM4001843, NT2RM4002352, NT2RP1000050, NT2RP1000181, NT2RP1000261, NT2RP1000300, NT2RP1000325, NT2RP1000448, NT2RP1000551, NT2RP1000613, NT2RP1000981, NT2RP1001004, NT2RP1001563, NT2RP2000479, NT2RP2000533, NT2RP2000616, NT2RP2000649, NT2RP2000663, NT2RP2000694, NT2RP2000818, NT2RP2000903, NT2RP2001200, NT2RP2001276, NT2RP2001480, NT2RP2001495, NT2RP2001514, NT2RP2001755, NT2RP2001915, NT2RP2001956, NT2RP2002063, NT2RP2002188, NT2RP2002232, NT2RP2002527, NT2RP2002533, NT2RP2002721, NT2RP2002824, NT2RP2002942, NT2RP2002976, NT2RP2003042, NT2RP2003210, NT2RP2003383, NT2RP2003390, NT2RP2003469, NT2RP2003593, NT2RP2003655, NT2RP2003664, NT2RP2003950, NT2RP2004179, NT2RP2004205, NT2RP2004495, NT2RP2004524, NT2RP2004556, NT2RP2004606, NT2RP2004648, NT2RP2004794, NT2RP2005027, NT2RP2005163, NT2RP2005181, NT2RP2005378, NT2RP2005463, NT2RP2005541, NT2RP2005597, NT2RP2005666, NT2RP2005883, NT2RP2005994, NT2RP2006004, NT2RP2006042, NT2RP2006269, NT2RP2006512, NT2RP2006580, NT2RP3000169, NT2RP3000171, NT2RP3000304, NT2RP3000436, NT2RP3000460, NT2RP3000616, NT2RP3000676, NT2RP3000721, NT2RP3000818, NT2RP3000907, NT2RP3000921, NT2RP3001012, NT2RP3001159, NT2RP3001195, NT2RP3001240, NT2RP3001271, NT2RP3001322, NT2RP3001388, NT2RP3001560, NT2RP3001592, NT2RP3001650, NT2RP3001738, NT2RP3001858, NT2RP3002015, NT2RP3002160, NT2RP3002311, NT2RP3002342, NT2RP3002411, NT2RP3002737, NT2RP3002790, NT2RP3002836, NT2RP3002900, NT2RP3002958, NT2RP3003000, NT2RP3003076, NT2RP3003354, NT2RP3003532, NT2RP3003535, NT2RP3003614, NT2RP3004025, NT2RP3004075, NT2RP3004083, NT2RP3004130, NT2RP3004133, NT2RP3004309, NT2RP3004345, NT2RP3004406, NT2RP3004481, NT2RP3004552, NT2RP3004625, NT2RP3004647, NT2RP4001001, NT2RP4001009, NT2RP4001467, NT2RP4001879, NT2RP4002187, NT2RP4002451, NT2RP4002750, OVARC1000003, OVARC1000105, OVARC1000298, OVARC1000307, OVARC1000313, OVARC1000410, OVARC1000439, OVARC1000553, OVARC1000811, OVARC1000873, OVARC1000956, OVARC1001030, OVARC1001163, OVARC1001336, OVARC1001570, OVARC1001607, OVARC1001725, OVARC1001991, PLACE1000033, PLACE1000231, PLACE1000560, PLACE1000740, PLACE1000912, PLACE1000914, PLACE1000927, PLACE1001016, PLACE1001123, PLACE1001183, PLACE1001231, PLACE1001340, PLACE1001401, PLACE1001407, PLACE1001464, PLACE1001516, PLACE1001536, PLACE1001564, PLACE1001655, PLACE1001795, PLACE1001836, PLACE1001918, PLACE1001949, PLACE1002080, PLACE1002095, PLACE1002355, PLACE1002374, PLACE1002518, PLACE1002547, PLACE1002726, PLACE1002905, PLACE1002911, PLACE1002967, PLACE1003407, PLACE1003573, PLACE1003737, PLACE1003772, PLACE1003839, PLACE1003845, PLACE1003852, PLACE1004279, PLACE1004282, PLACE1004441, PLACE1004450, PLACE1004482, PLACE1004520, PLACE1004630, PLACE1004637, PLACE1004648, PLACE1004816, PLACE1005003, PLACE1005005, PLACE1005031, PLACE1005383, PLACE1005410, PLACE1005426, PLACE1005544, PLACE1005569, PLACE1005660, PLACE1005725, PLACE1005745, PLACE1005878, PLACE1005927, PLACE1006071, PLACE1006093, PLACE1006208, PLACE1006277, PLACE1006290, PLACE1006443, PLACE1006716, PLACE1006809, PLACE1006959, PLACE1007081, PLACE1007096, PLACE1007296, PLACE1007626, PLACE1007845, PLACE1007881, PLACE1008359, PLACE1008469, PLACE1008716, PLACE1008744, PLACE1008985, PLACE1009067, PLACE1009196, PLACE1009279, PLACE1009527, PLACE1009546, PLACE1009600, PLACE1009982, PLACE1010011, PLACE1010078, PLACE1010251, PLACE1010445, PLACE1010713, PLACE1010784, PLACE1010827, PLACE1010968, PLACE1011116, PLACE1011181, PLACE1011236, PLACE1011516, PLACE1011708, PLACE3000181, PLACE3000213, PLACE4000354, SKNMC1000004, SKNMC1000014, SKNMC1000082, THYRO1000036,

THYRO1000099, THYRO1000196, THYRO1000400, THYRO1000584, THYRO1000678, THYRO1000776, THYRO1000795, THYRO1000956, THYRO1001102, THYRO1001113, THYRO1001205, THYRO1001237, THYRO1001242, THYRO1001266, THYRO1001327, THYRO1001456, THYRO1001478, THYRO1001523, THYRO1001529, THYRO1001641, THYRO1001702, THYRO1001725, Y79AA1000207, Y79AA1000226, Y79AA1000270, Y79AA1000426, Y79AA1000521, Y79AA1000876, Y79AA1000888, Y79AA1000959, Y79AA1001013, Y79AA1001212, Y79AA1001264, Y79AA1001328, Y79AA1001426, Y79AA1001427, Y79AA1001430, Y79AA1001727, Y79AA1001787, Y79AA1001795, Y79AA1001799, Y79AA1001803, Y79AA1002022, Y79AA1002058, Y79AA1002129, Y79AA1002213, Y79AA1002373,

[0251] The following 146 clones were categorized into glycoprotein-associated proteins.

BNGH41000087, BNGH41000091, HEMBA1000349, HEMBA1000590, HEMBA1000745, HEMBA1000835, HEMBA1001221, HEMBA1001228, HEMBA1001621, HEMBA1002131, HEMBA1002178, HEMBA1002421, HEMBA1002767, HEMBA1003230, HEMBA1003392, HEMBA1004250, HEMBA1004391, HEMBA1004444, HEMBA1004505, HEMBA1005449, HEMBA1005522, HEMBA1005545, HEMBA1006707, HEMBA1006749, HEMBA1006902, HEMBB1000679, HEMBB1000881, HEMBB1001048, HEMBB1002120, HEMBB1002245, HEMBB1002427, MAMMA1000102, MAMMA1000591, MAMMA1000681, MAMMA1001043, MAMMA1001237, MAMMA1002070, MAMMA1002586, MAMMA1003126, NT2RM1000462, NT2RM1000580, NT2RM2001792, NT2RM2001818, NT2RM2001939, NT2RM2001941, NT2RM4000198, NT2RM4000284, NT2RM4000417, NT2RM4000648, NT2RM4000997, NT2RM4001325, NT2RM4002352, NT2RP1000613, NT2RP1000981, NT2RP1001004, NT2RP2000616, NT2RP2000694, NT2RP2000903, NT2RP2001480, NT2RP2001755, NT2RP2002533, NT2RP2003042, NT2RP2003210, NT2RP2004205, NT2RP2004606, NT2RP2005027, NT2RP2005181, NT2RP2005541, NT2RP2005597, NT2RP2005883, NT2RP2006004, NT2RP2006042, NT2RP2006269, NT2RP3000304, NT2RP3000616, NT2RP3000921, NT2RP3001650, NT2RP3002160, NT2RP3002737, NT2RP3002958, NT2RP3003000, NT2RP3003532, NT2RP3004130, NT2RP3004133, NT2RP3004481, NT2RP3004552, NT2RP3004640, NT2RP4000108, NT2RP4001467, NT2RP4002750, OVARC1000003, OVARC1000553, OVARC1000811, OVARC1000873, OVARC1001336, OVARC1001607, OVARC1001991, PLACE1000033, PLACE1000740, PLACE1001016, PLACE1001123, PLACE1001231, PLACE1001464, PLACE1001655, PLACE1001836, PLACE1002355, PLACE1002374, PLACE1002905, PLACE1002911, PLACE1003573, PLACE1003737, PLACE1003772, PLACE1003839, PLACE1004282, PLACE1004441, PLACE1004450, PLACE1004520, PLACE1004648, PLACE1005003, PLACE1005426, PLACE1006071, PLACE1006073, PLACE1006290, PLACE1007081, PLACE1007845, PLACE1008716, PLACE1008744, PLACE1008985, PLACE1010251, PLACE1010784, PLACE1010968, PLACE1011116, PLACE3000181, PLACE3000213, PLACE4000354, THYRO1000036, THYRO1000196, THYRO1000584, THYRO1000956, THYRO1001266, Y79AA1000270, Y79AA1000426, Y79AA1001727, Y79AA1001795, Y79AA1002022, Y79AA1002213,

[0252] The following 55 clones were categorized into signal transduction-associated proteins.

HEMBA1000006, HEMBA1002195, HEMBA1002227, HEMBA1002551, HEMBA1005084, HEMBA1005929, HEMBA1006658, HEMBA1006916, MAMMA1000881, MAMMA1001150, MAMMA1001310, MAMMA1002142, NT2RM2001902, NT2RP1001020, NT2RP1001031, NT2RP2001469, NT2RP2001529, NT2RP2001769, NT2RP2003179, NT2RP2003545, NT2RP2004670, NT2RP3000011, NT2RP3000022, NT2RP3000172, NT2RP3000201, NT2RP3000820, NT2RP3003527, NT2RP3003849, NT2RP3003874, NT2RP3004067, NT2RP4000634, NT2RP4000962, OVARC1000255, OVARC1000529, OVARC1000916, OVARC1001338, OVARC1001569, PLACE1002329, PLACE1003135, PLACE1003598, PLACE1005519, PLACE1006208, PLACE1008282, PLACE1008297, PLACE1010081, PLACE1011364, PLACE1011824, THYRO1001457, THYRO1001593, THYRO1001700, THYRO1001770, Y79AA1000777, Y79AA1000967, Y79AA1002376, Y79AA1002381,

[0253] The following 80 clones were categorized into transcription -associated proteins.

HEMBA1000462, HEMBA1000671, HEMBA1001297, HEMBA1001390, HEMBA1001886, HEMBA1002048, HEMBA1003120, HEMBA1003497, HEMBA1004785, HEMBA1005230, HEMBA1005246, HEMBA1006276, HEMBA1006572, HEMBA1007226, HEMBB1000106, HEMBB1000905, HEMBB1001959, HEMBB1002051, HEMBB1002661, MAMMA1001094, MAMMA1001532, MAMMA1001615, NT2RM1000789, NT2RM2000632, NT2RM2000773, NT2RM4000326, NT2RP1000271, NT2RP1000468, NT2RP2000092, NT2RP2000610, NT2RP2000712, NT2RP2000739, NT2RP2001538, NT2RP2001662, NT2RP2001817, NT2RP2001948, NT2RP2002564, NT2RP2002974, NT2RP2003138, NT2RP2003302, NT2RP2003940, NT2RP2004108, NT2RP2004847, NT2RP2005247, NT2RP2005391, NT2RP2005535, NT2RP2005774, NT2RP2005941, NT2RP2006092, NT2RP3000148, NT2RP3000232, NT2RP3000378, NT2RP3000652, NT2RP3001976, NT2RP3004090, NT2RP3004119, NT2RP3004294, OVARC1001049, OVARC1001086, OVARC1001132, OVARC1001807, PLACE1000258, PLACE1000442, PLACE1000907, PLACE1003529, PLACE1004166,

PLACE1004168, PLACE1004887, PLACE1005250, PLACE1005682, PLACE1006079, PLACE1008549, PLACE1011407, PLACE1011978, THYRO1000580, Y79AA1000030, Y79AA1001090, Y79AA1001523, Y79AA1002334, Y79AA1002378,

[0254] The following 85 clones were categorized into disease-associated proteins.

BNGH41000020, HEMBA1000349, HEMBA1000590, HEMBA1000671, HEMBA1000835, HEMBA1001184, HEMBA1001228, HEMBA1001886, HEMBA1003120, HEMBA1004250, HEMBA1005246, HEMBA1005267, HEMBA1006707, HEMBA1006749, HEMBA1006902, HEMBA1006916, HEMBA1007013, HEMBB1002120, MAMMA1000204, MAMMA1002080, NT2RM2000632, NT2RM2001126, NT2RM2001558, NT2RP1000271, NT2RP1000465, NT2RP1000579, NT2RP2000447, NT2RP2000514, NT2RP2000739, NT2RP2001223, NT2RP2001529, NT2RP2001562, NT2RP2002674, NT2RP2003369, NT2RP2004108, NT2RP2004205, NT2RP2005535, NT2RP2005941, NT2RP2006004, NT2RP3000059, NT2RP3000125, NT2RP3000201, NT2RP3000232, NT2RP3000616, NT2RP3000677, NT2RP3000838, NT2RP3000921, NT2RP3001542, NT2RP3002286, NT2RP3002721, NT2RP3002737, NT2RP3002738, NT2RP3004481, OVARC1000208, OVARC1000275, OVARC1000331, OVARC1000410, OVARC1001086, OVARC1001132, OVARC1001607, OVARC1001725, OVARC1001952, PLACE1000258, PLACE1000442, PLACE1000907, PLACE1001100, PLACE1001500, PLACE1002905, PLACE1002967, PLACE1003407, PLACE1003428, PLACE1005005, PLACE1005239, PLACE1005815, PLACE1007028, PLACE1008716, PLACE1011407, PLACE1011978, PLACE2000118, THYRO1000580, THYRO1000866, THYRO1001071, THYRO1001478, Y79AA1001062, Y79AA1001530,

[0255] Out of them, the following 67 clones are those which matched the data of Swiss-Prot database and GenBank or UniGene database, genes or proteins which had been deposited in the database of Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nim.nih.gov/Omim/), which is a database of human genes and diseases. (The corresponding OMIM numbers are indicated after the clone names.)

HEMBA1000349(*600046), HEMBA1000590(*603897), HEMBA1000671(*602277), HEMBA1001886(*603899), HEMBA1003120(*602277), HEMBA1004250(*600976), HEMBA1005246(*602291), HEMBA1005267(*106410), HEMBA1006707(*603897), HEMBA1006749(*603897), HEMBA1006902(*603897), HEMBA1006916(*601524), HEMBA1007013(*603730), HEMBB1002120(*603367), MAMMA1002080(*602672), NT2RM2001126(*603785), NT2RM2001558(*604689), NT2RP1000271(*603899), NT2RP1000465(*602231), NT2RP2000447(*602580), NT2RP2000514(*602431), NT2RP2000739(*194558), NT2RP2001223(*603558), NT2RP2001529(*603289), NT2RP2001562(*603371), NT2RP2002674(*132811), NT2RP2003369(*179555), NT2RP2004108(*601260), NT2RP2004205(*601610), NT2RP2005535(*603899), NT2RP2006004(*600245), NT2RP3000059(*106410), NT2RP3000125(*180202), NT2RP3000201(*604666), NT2RP3000232(*602277), NT2RP3000616(*600245), NT2RP3000677(*142765), NT2RP3000838(*190370), NT2RP3001542(*191161), NT2RP3002286(*604331), NT2RP3002721(*118950), NT2RP3002738(*602265), NT2RP3004481(*601610), OVARC1000208(*603603), OVARC1000275(*125647), OVARC1000331(*139265), OVARC1000410(*603874), OVARC1001086(*603862), OVARC1001725(*603046), OVARC1001952(*190370), PLACE1000258(*603971), PLACE1000442(*601260), PLACE1000907(*194558), PLACE1001500(*603781), PLACE1002905(*125950), PLACE1003428(*603570), PLACE1005005(*603124), PLACE1005239(*603365), PLACE1007028(*602131), PLACE1011407(*602277), PLACE1011978(*603971), PLACE2000118(*301000), THYRO1000580(*602277), THYRO1000866(*604045), THYRO1001071(*603533), Y79AA1001062(*191161), Y79AA1001530(*602662),

[0256] Out of 215 clones excluding the above-mentioned clones, HEMBB1000668 and NT2RM4001377 presumably belong to a group of signal transduction-associated proteins, based on the results of domain search by Pfam.

[0257] HEMBB1002302 presumably belong to a group of transcription-associated proteins, based on the results of domain search by Pfam.

[0258] In the 437 clones categorized into secretory and/or transmembrane proteins on the basis of their full-length sequences, 410 clones were also predicted to encode proteins having functions of secretory and/or membrane proteins on the basis of their partial nucleotide sequences (5' sequences). In the 146 clones categorized into glycoprotein-associated proteins on the basis of their full-length sequences, 124 clones were also predicted to encode proteins having functions of glycoprotein-associated proteins on the basis of their partial nucleotide sequences. In the 57 clones categorized into signal transduction-associated proteins on the basis of their full-length sequences, 46 clones were also predicted to encode proteins having functions of signal transduction-associated proteins on the basis of their partial nucleotide sequences. In the 81 clones categorized into transcription-associated proteins on the basis of their full-length sequences, 57 clones were also predicted to encode proteins having functions of transcription-associated proteins on the basis of their partial nucleotide sequences. In the 85 clones categorized into disease-associated proteins on the basis of their full-length sequences, 6 clones were also predicted to encode proteins having functions of disease-associated proteins on the basis of their partial nucleotide sequences. The number of clones which were predicted to encode disease-associated proteins based on the full-length nucleotide sequences is much greater than that predicted based on the partial sequences. The reason is that the full-length sequences were categorized by using the data found

in the OMIM database into the category of disease-associated proteins.

[0259] When the predicted functions based on the partial sequences were different from those based on the full-length sequences, several reasons were presumed; the ORF is too short in the partial sequence as compared with that of the full-length sequence; alternatively, P value for the partial sequence was greater than that for the full-length, that is, as compared with the probability of occurrence of the predicted function found in the full-length sequence, the probability was lower in the partial sequence. A protein does not always belong solely to a single category of the above-described functional categories, and therefore, additional functions can be found for the cDNA clones by further analyses.

[0260] It is unclear, by the analyses for the full-length sequences so far, whether or not the remaining 212 clones encode proteins belonging to any of the categories of secretory and/or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins or disease-associated proteins. Nonetheless, the functions which were predicted based on the partial sequences can be verified by further analyses.

[0261] Among the 212 clones, there are 38 clones that presumably belong to the category of enzymes and/or metabolism-associated proteins, cell division- and/or cell proliferation-associated proteins, cytoskeleton-associated proteins, nuclear proteins, DNA-and/or RNA-binding proteins, ASP- and/or GTP-binding proteins, protein synthesis- and/or protein transport-associated proteins, or cellular defense-associated proteins. The clones containing results of homology search of Swiss-Prot database were categorized by considering the keywords and mentioned items in the matching data. The clones containing results of homology search of GenBank or UniGene database were categorized by considering the definitions and mentioned items in the matching data.

When the matching data contained keywords such as "metabolism", "oxidoreductase" and "E.C. No. (Enzyme commission number)", the clones were herein defined as clones presumably belonging to the category of enzymes and/or metabolism-associated proteins. When the matching data contained keywords such as "cell division", "cell cycle", "mitosis", "chromosomal protein", "cell growth" and "apoptosis", the clones were herein defined as clones presumably belonging to the category of cell division- or cell proliferation-associated proteins. When the matching data contained keywords such as "structural protein", "cytoskeleton", "actin-binding" and "microtubules", the clones were herein defined as clones presumably belonging to the category of cytoskeleton-associated proteins. When the matching data contained keywords such as "nuclear protein", the clones were herein defined as clones presumably belonging to the category of nuclear proteins. When the matching data contained keywords such as "DNA-binding" and "RNA-binding", the clones were herein defined as clones presumably belonging to the category of DNA- or RNA-binding proteins. When the matching data contained keywords such as "ATP-binding" and "GTP-binding", the clones were herein defined as clones presumably belonging to the category of ATP- and/or GTP-binding proteins. When the matching data contained keywords such as "translation regulation", "protein biosynthesis", "amino-acid biosynthesis", "ribosomal protein", "protein transport" and "signal recognition particle", the clones were herein defined as clones presumably belonging to the category of protein synthesis- and/or protein transport-associated proteins. When the matching data contained keywords such as "heat shock", "DNA repair" and "DNA damage", the clones were herein defined as clones presumably belonging to the category of cellular defense-associated proteins.

[0262] The following 10 clones presumably belong to enzymes and/or metabolism-associated proteins.
HEMBA1003315, HEMBB1002465, MAMMA1000614, NT2RP2000178, NT2RP2001388, NT2RP2001903, NT2RP2002304, NT2RP2005878, NT2RP3001685, PLACE1006219

[0263] The following 4 clones presumably belong to cell division-associated and/or cell proliferation-associated proteins.
MAMMA1000403, NT2RM2000497, NT2RP2000394, Y79AA1002121

[0264] The following 6 clones presumably belong to cytoskeleton-associated proteins.
MAMMA1001609, NT2RM2000589, NT2RP3000063, PLACE1004078, PLACE 1004492, PLACE 1008657

[0265] The following 7 clones presumably belong to nuclear proteins.
HEMBA1001878, HEMBA1002992, MAMMA1000614, NT2RM4000965, NT2RM2001738, NT2RP2001388, Y79AA1002121

[0266] The following 5 clones presumably belong to DNA- and/or RNA-binding proteins.
HEMBA1003072, HEMBA1006770, HEMBA1007332, NT2RM2000497, Y79AA1002121

[0267] The following 7 clones presumably belong to ATP- and/or GTP-binding proteins.
HEMBA1002316, MAMMA1001609, NT2RM2000306, NT2RM2000497, NT2RP2000178, NT2RP3003729, PLACE1004305

[0268] The following 7 clones presumably belong to protein synthesis- and/or protein transport-associated proteins.
NT2RM4000965, NT2RP2005069, NT2RP3000481, NT2RP3000789, NT2RP4001877, OVARC1001833, OVARC1002058,

[0269] The following clone presumably belongs to cellular defense-associated proteins.
PLACE 1005539

[0270] Although it is unclear whether or not 26 out of 174 clones other than the above-mentioned clones belong to

any of the above-described categories, these clones are predicted to have some functions, based on the homology search using their full-length sequences. The clone names and the gene definitions found in the result of homology search are shown below, separated by a double-slash,//

HEMBA1000634//Homo sapiens T-cell activation protein (PGR1) gene, complete cds.
HEMBA1002524//Human MHC Class I region proline rich protein mRNA, complete cds.
HEMBA1003399//MVP1 PROTEIN,
HEMBA1005489//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds.
HEMBB1000542//Mus musculus bromodamain-containing protein BP75 mRNA, complete cds.
MAMMA1000788//Bos taurus P14 (p14) mRNA, complete cds.
MAMMA1002128//ABC1 PROTEIN HOMOLOG PRECURSOR.
NT2RM2000514//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.
NT2RM2000622//Mus musculus F-box protein FBL10 mRNA, partial cds.
NT2RM4000100//Homo Sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.
NT2RP2005425//Homo sapiens mRNA for AKAP450 protein.
NT2RP3001170//Mus musculus activity-dependent neuroprotective protein (Adnp) mRNA, complete cds.
NT2RP3002571//Bos taurus mRNA for lyncein.
NT2RP3004557//Human Ki nuclear autoantigen mRNA, complete cds.
OVARC1001596//Homo sapiens Arf-like 2 binding protein BART1 mRNA, complete cds.
PLACE1002153//Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.
PLACE1003163//Homo sapiens DBI-related protein mRNA, complete cds.
PLACE1005736//Human mRNA for BAS-GRIP protein.
PLACE1007702//Mus musculus TRA1 mRNA, complete cds.
PLACE1011045//Homo sapiens E1-like protein mRNA, complete cds.
THYRO1000061//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.
THYRO1000964//Drosophila melanogaster Felle associated protein Pellino (Pli) mRNA, complete cds.
Y79AA1000776//Mus musculus mRNA for GSG1, complete cds.
Y79AA1001056//Homo sapiens MAID protein mRNA, complete cds.
Y79AA1001272//Homo sapiens retinoic acid repressible protein (RARG-1) mRNA, complete cds.
Y79AA1001793//Mus musculus mRNA for GSG1, complete cds.

[0271] So far, useful information for presuming the functions are unavailable for the remaining 148 clones, of which names are listed below.

HEMBA1000275, HEMBA1000300, HEMBA1000443, HEMBA1000875, HEMBA1000907, HEMBA1001272, HEMBA1001296, HEMBA1001563, HEMBA1002164, HEMEA1002239, HEMBA1002985, HEMBA1003294, HEMBA1003487, HEMBA1004007, HEMBA1004067, HEMBA1004085, HEMBA1004952, HEMBA1004971, HEMBA1005145, HEMBA1005430, HEMBA1005913, HEMBA1006016, HEMBA1006517, HEMBA1006544, HEMBA1006912, HEMBA1007057, HEMBA1007063, HEMBA1007291, HEMBB1000276, HEMBB1000309, HEMBB1000642, HEMBB1001200, HEMBB1001547, HEMBB1002039, HEMBB1002228, HEMBB1002663, MAMMA1000046, MAMMA1000449, MAMMA1000528, MAMMA1000652, MAMMA1000706, MAMMA1000814, MAMMA1001066, MAMMA1001284, MAMMA1001623, MAMMA1001634, MAMMA1001901, MAMMA1002087, MAMMA1002205, MAMMA1002224, NT2RM2000582, NT2RM2001643, NT2RM4000115, NT2RM4000295, NT2RM4001321, NT2RP1000002, NT2RP1000239, NT2RP1000679, NT2RP1000740, NT2RP1000903, NT2RP2000240, NT2RP2001878, NT2RP2001921, NT2RP2002015, NT2RP2002409, NT2RP2002510, NT2RP2003599, NT2RP2003931, NT2RP2004069, NT2RP2004141, NT2RP2004447, NT2RP2004837, NT2RP2005514, NT2RP2005632, NT2RP2005887, NT2RP2006099, NT2RP2006134, NT2RP3000427, NT2RP3000444, NT2RP3000645, NT2RP3000871, NT2RP3001044, NT2RP3001061, NT2RP3001754, NT2RP3002281, NT2RP3002324, NT2RP3002353, NT2RP3002409, NT2RP3002448, NT2RP3002664, NT2RP3002887, NT2RP3002983, NT2RP3003448, NT2RP3003469, NT2RP3003473, NT2RP3003559, NT2RP3003963, NT2RP3004000, NT2RP3004202, NT2RP3004321, NT2RP3004355, NT2RP3004374, NT2RP4002715, OVARC1000090, OVARC1000137, OVARC1000467, OVARC1000775, OVARC1000853, OVARC1000995, OVARC1001222, OVARC1001260, OVARC1001727, OVARC1002178, PLACE1000986, PLACE1001114, PLACE1001229, PLACE1001788, PLACE1003438, PLACE1003460, PLACE1003644, PLACE1004028, PLACE1004199, PLACE1004519, PLACE1005601, PLACE1005669, PLACE1005768, PLACE1006515, PLACE1006786, PLACE1007040, PLACE1007077, PLACE1007591, PLACE1007971, PLACE1008984, PLACE1009735, PLACE2000219, PLACE4000455, THYRO1000846, THYRO1000999, THYRO1001063, THYRO1001128, THYRO1001471, THYRO1001495,

THYRO1001608, THYRO1001803, Y79AA1000127, Y79AA1000750, Y79AA1001592, Y79AA1001863,

EXAMPLE 18

Expression frequency analysis using PCR

[0272] Many genes acting at the downstream of TNF-. and IL-1. among inflammation-associated cytokines have been previously identified. The respective stimulations are transduced through independent pathways of signaling cascade. There exists another signaling cascade for both stimulations, wherein NF-.B is a common transducing molecule shared by the two stimulations (J. Leukoc. Biol., 1994, 56(5): 542-547). It has also been revealed that many inflammation-associated genes, including IL-2, IL-6 and G-CSF, are varied in their expression levels in response to the signal through the common pathway (Trends Genet. 1999, 15(6): 229-235). A survey was performed by using ATAC-PCR method (adaptor-competitive PCR method: Nucleic Acids Res. 1997, Nov 15; 25(22): 4694-6) for genes of which expression levels were varied depending on stimulation of inflammatory cytokines, TNF-. and IL-1.. It is possible that genes of which expression is varied in response to this stimulation also participate in inflammation.

[0273] Jurkat cells (Dainippon Pharmaceutical Co., Ltd.: catalog No. 06-152) were cultured in a PRMI1640 medium (Nikken Biological and Medical Institute: catalog No. 14-501F) containing 10% fetal calf serum until the cell count reached 10^7 cells. The cells were transferred into a fresh medium containing 10 ng/ml TNF-. (recombinant Tumor Necrosis Factor; Wako pure chemical Industries Inc.: catalog No. 201-13461) or IL-1. (recombinant Interleukin-1.; PeprotechEC: catalog No. 200-01B) and, further, cultured at 37. under an atmosphere of 5% CO_2. The cells cultured in the presence of TNF-. were harvested 1, 3 and 7 hours after addition of TNF-.. The cells cultured in the presence of IL-1. were harvested 1 and 7 hours after addition of IL-1.. Total RNA was extracted from each of the cells by AGPC method (Acid-Guanidinium-Phenol-Chloroform method: Ana Biochem. 1987, Apr; 162(1):156-9). Total RNA was also extracted form the cells in the absence of any stimulation of TNF-. and IL-1

[0274] ATAC-PCR analysis is performed basically according to the same procedure as described in "DNA Microarray and Advanced PCR Methods" (Cell Engineering, p. 104-112, (additional volume, Genome Science Series 1), Muramatsu & Naba (eds.), Shujunnsya). Adaptor ligation reaction was performed for an internal standard sample (which was used for preparing a calibration curve for the assessment of the test samples) and test samples in the following independent two reaction systems. Combinations of each type of the 6 adaptors (AD-1, AD-2, AD-3, AD-4, AD-5, and AD-6: see the sequences shown below) with each sample are as follows:

Reaction system A

AD1: internal standard sample (x10 concentration)
AD2: sample before stimulation
AD3: internal standard sample (x3 concentration)
AD4: sample with IL-1 stimulation for 1 hour
AD5: sample with IL-1 stimulation for 7 hours
AD6: internal standard sample (x1 concentration)

Reaction system B

AD1: internal standard sample (x1 concentration)
AD2: sample with TNF stimulation for 1 hour
AD3: sample with TNF stimulation for 3 hours
AD4: internal standard sample (x3 concentration)
AD5: sample with TNF stimulation for 7 hours
AD6: internal standard sample (x10 concentration)

Adaptor sequence

AD1;

SEQ ID NO:4180//5'-GTACATATTGTCGTTAGAACGCG-3'

SEQ ID NO:4181//3'-CATGTATAACAGCAATCTTGCGCCTAG-5'

AD2;

SEQ ID NO:4182//5'-GTACATATTGTCGTTAGAACGCGACT-3'

SEQ ID NO:4183//3'-CATGTATAACAGCAATCTTGCGCTGACTAG-5'

AD3;

SEQ ID NO:4184//5'-GTACATATTGTCGTTAGAACGCGCATACT-3'

SEQ ID NO:4185//3'-CATGTATAACAGCAATCTTGCGCGTATCACTAG-5'

AD4;

SEQ ID NO:4186//5'-GTACATATTGTCGTTAGAACGCGATCCATACT-3'

SEQ ID NO:4187//3'-CATGTATAACAGCAATCTTGCGCTAGGTATGACTAG-5'

AD5;

SEQ ID NO:4188//5'-GTACATATTGTCGTTAGAACGCGTCAATCCATACT-3'

SEQ ID NO:4189//3'-CATGTATAACAGCAATCTTGCGCAGTTAGGTATGACTAG-5'

AD6;

SEQ ID NO:4190//5'-GTACATATTGTCGTTAGAACGCGTACTCAATCCATACT-3'

SEQ ID NO:4191//3'-CATGTATAACAGCAATCTTGCGCATGAGTTAGGTATGACTAG-5'

[0275] In this assay, the internal standard samples used were total RNA from cultured cells or human tissues from which the cDNA libraries originated. The cultured cells and the total RNAs from tissues are indicated below. Culture of the cells was performed according to the method as described in the supplier's instruction manual. RNA preparation was carried out by standard methods.

Human teratocarcinoma cell NT-2 (Stratagene, catalog No. 204101)
Human neuroblastoma cell SK-N-MC (Dainippon Pharmaceutical Co., Ltd., catalog No. 04-010)
Human neuroblastoma cell Y79 (Dainippon Pharmaceutical Co., Ltd., catalog No. 04-018)
Human placenta tissues total RNA (BioChin, catalog No. 064008)
Human breast tissue total RNA (Clontech, catalog No. 64037-1)

[0276] PCR primers used for amplification of specific genes, and names of the corresponding cDNA clones are shown below. The assay was not carried out for clones of which corresponding internal standard sample could not be prepared for the assay. The gene-specific primers were designed so that the PCR products derived from the cDNAs with adaptor were 70-200 bp in size. Sequence of the adaptor-specific primer (labeled with fluorescent dye (FAM)) used for the competitive PCR was GTACATATTGTCGTTAGAACGC (22 nucleotides, SEQ ID NO: 4192). PCR was performed basically at 94. for 5 minutes; and at 94. for 30 seconds, at 50. for 60 seconds, and at 72. for 60 seconds for 30 cycles. The annealing temperature was, however, changed in some PCR experiments.

[0277] Nucleotide sequence of clone-specific primer (all the primers consist of 20 nucleotides) used in this experiment

[0278] Clone names, primer sequences, and SEQ ID NOs were shown in this order, separated with a double-slash mark, //

MAMMA1000046//GTTACATCCAAGCATACAGG//SEQ ID NO:4193
MAMMA1000102//ACGGGGTCTCATTCTGACAC//SEQ ID NO:4194
MAMMA1000141//CAAGGTAACACGAGTCTATC//SEQ ID NO:4195
MAMMA1000226//ACTGAGGGGCAAAGGAGAGA//SEQ ID NO:4196
MAMMA1000403//ATTTTCCTGGAGAGCCGACT//SEQ ID NO:4197
MAMMA1000473//TGGAAAGTGTACCGGAATTG//SEQ ID NO:4198
MAMMA1000496//TCAATCTGGCGCTCTGTCAC//SEQ ID NO:4199
MAMMA1000614//AGTTCTTTACATGCTGAGGT//SEQ ID NO:4200
MAMMA1000652//TGGTGGAAGACTGGGTTTGC//SEQ ID NO:4201
MAMMA1000706//ATGGTCTTGTGGTGCCAGGT//SEQ ID NO:4202
MAMMA1000788//TGTCCAAAAGCCACACAGAG//SEQ ID NO:4203
MAMMA1000810//ATACTTCCCGCACCCCAAAA//SEQ ID NO:4204
MAMMA1000814//CAGGGTTTCTGCATGTTGGC//SEQ ID NO:4205
MAMMA1000881//ATGGAGTTTCACTCTTGTTG//SEQ ID NO:4206
MAMMA1000986//TGCTGCTTCTTTACATGGGA//SEQ ID NO:4207
MAMMA1000994//CAGGATAGAGGTTGCAGGCT//SEQ ID NO:4208
MAMMA1001066//GATGGGGTCTCACTCTGTCA//SEQ ID NO:4209
MAMMA1001094//ACGTCCAGAAACTACAGGGT//SEQ ID NO:4210
MAMMA1001141//ACTGTACTTAGGATGCTTCA//SEQ ID NO:4211
MAMMA1001237//GGGCAACCCTATGTAGATGA//SEQ ID NO:4212
MAMMA1001284//GTCTGCTCTGTTACATAGGG//SEQ ID NO:4213
MAMMA1001310//ACGCCTGTAATCCCAACCCA//SEQ ID NO:4214
MAMMA1001344//GCCAGTTTGTTCTAGGATGC//SEQ ID NO:4215
MAMMA1001532//ACATCTATAAGGCTGTTTGC//SEQ ID NO:4216
MAMMA1001609//GGGTCTCACTCTGTTACCCA//SEQ ID NO:4217
MAMMA1001615//CAAGGGACACTGAGAACTGG//SEQ ID NO:4218
MAMMA1001623//GGATTGATGCCCGATACTTA//SEQ ID NO:4219
MAMMA1001901//GATAGGGTCTCATTCTGTTA//SEQ ID NO:4220
MAMMA1001957//TAGTAGAGACGGGGTTTCAC//SEQ ID NO:4221
MAMMA1001978//CTCCCTCAGACGCTTTATTG//SEQ ID NO:4222
MAMMA1002070//GAAGAGAAACTGGGGCATCC//SEQ ID NO:4223
MAMMA1002080//ACTCTCCCTCACTACCACTG//SEQ ID NO:4224
MAMMA1002087//AGCTCGTCTCATGGGCAACT//SEQ ID NO:4225
MAMMA1002091//CTGACGTAGGTGAGGTCCAT//SEQ ID NO:4226

MAMMA1002095//CATGTTTATGGTCAGGTAGT//SEQ ID NO:4227
MAMMA1002128//TGGAGCAGATGAGGAAGGAG//SEQ ID NO:4228
MAMMA1002142//TCTCTTAAACATGCAACAGG//SEQ ID NO:4229
MAMMA1002165//CTCAAACACCCAGGCTCAAG//SEQ ID NO:4230
MAMMA1002234//TTTGTCTTCCTCTAAACCAG//SEQ ID NO:4231
MAMMA1002586//CTCCACCGAAAAGACCCATT//SEQ ID NO:4232
MAMMA1002633//CACAGCAGCATCTCCAAGCA//SEQ ID NO:4233
MAMMA1003126//ACAGTATCAGAGGAGCAGGA//SEQ ID NO:4234
NT2RM1000462//AGAGCCGAGGACATTTGAGG//SEQ ID NO:4235
NT2RM1000542//CAAGGGCACGTTTCAGCACT//SEQ ID NO:4236
NT2RM1000789//TTCGCTTGCTCTTCTCTGGA//SEQ ID NO:4237
NT2RM1000855//AGCAAGGTCTCCAGAGTGTG//SEQ ID NO:4238
NT2RM1000858//GAACAGGAAAATGCTCTCAG//SEQ ID NO:4239
NT2RM2000241//CTGCTTGCCTGCCTTGTAGT//SEQ ID NO:4240
NT2RM2000306//TAGTCCCTTTCCTGATGGTC//SEQ ID NO:4241
NT2RM2000497//TTAGTAGAGACGGTGTTTCA//SEQ ID NO:4242
NT2RM2000514//TGTTCTCTTTCTTTGCACTG//SEQ ID NO:4243
NT2RM2000582//GGGAATAACATCTACAACCT//SEQ ID NO:4244
NT2RM2000588//CCCCAGAAACAGAGAAGGCT//SEQ ID NO:4245
NT2RM2000589//TAAGGCATGTGTCCTCTAAG//SEQ ID NO:4246
NT2RM2000622//ATCTCGGCTATGAACTGCTC//SEQ ID NO:4247
NT2RM2000773//TTCTGCCCCTCCTCAAACCT//SEQ ID NO:4248
NT2RM2001126//GCAACAGCTTCTTCATGGGT//SEQ ID NO:4249
NT2RM2001558//TCGCCCACACTGCATCCTTT//SEQ ID NO:4250
NT2RM2001626//TCGGGTGGCAGTGTGTTGAA//SEQ ID NO:4251
NT2RM2001643//GTAGTTCTCTCTGAAGAATC//SEQ ID NO:4252
NT2RM2001738//CCCAGCACTTTTATTTGTAG//SEQ ID NO:4253
NT2RM2001792//AGTGTAGTTTGGAGATGAGA//SEQ ID NO:4254
NT2RM2001902//TCCCCATCCAGCCACAGAAA//SEQ ID NO:4255
NT2RM2002109//ATTGCCTATAGAAAGTCAGC//SEQ ID NO:4256
NT2RM4000100//GCATTTATAGGGCTCAAGAT//SEQ ID NO:4257
NT2RM4000115//TAGTTTCGACTTCTGGTTCA//SEQ ID NO:4258
NT2RM4000284//ACATCCTTCAAATCAGCATC//SEQ ID NO:4259
NT2RM4000295//GGTCTCACGCTGCTCACAAA//SEQ ID NO:4260
NT2RM4000417//TGCTGTGTAGTATTCCTTAG//SEQ ID NO:4261
NT2RM4000761//CTAATACAATGCCAGTCAGG//SEQ ID NO:4262
NT2RM4001377//CTAGCTTCCTCTCCCAACTG//SEQ ID NO:4263
NT2RM4001735//TCATCACGACTGCTGTAGAG//SEQ ID NO:4264
NT2RM4001768//TTAGTAGACGTGGGGTTTCA//SEQ ID NO:4265

NT2RM4001843//CAAGGGCACGTTTCAGCACT//SEQ ID NO:4266
NT2RP1000239//TTAGCAGTGTATCCTTTCCG//SEQ ID NO:4267
NT2RP1000465//TTGCCCAGGCTAGTCTCGAA//SEQ ID NO:4268
NT2RP1000468//TTGCCCAGGCTAGTCTCGAA//SEQ ID NO:4269
NT2RP1000679//GGCCTCAGTTCCTTGCATTT//SEQ ID NO:4270
NT2RP1000740//CGCTATATTTCATGGGCTTT//SEQ ID NO:4271
NT2RP1001031//CATGTTACCTATACACACCA//SEQ ID NO:4272
NT2RP2000092//CACACACACATGAACTCATT//SEQ ID NO:4273
NT2RP2000178//ATCTTTTGTGACAGCTCCAG//SEQ ID NO:4274
NT2RP2000240//CCATTCCACTCATACCAAGA//SEQ ID NO:4275
NT2RP2000447//CTCTTGGCATGATAGGTCTT//SEQ ID NO:4276
NT2RP2000610//GACATGAGACAAAATTAGCC//SEQ ID NO:4277
NT2RP2000616//AAAATAACTGCCTGGGAGGT//SEQ ID NO:4278
NT2RP2000712//GAAGGTAGAGCTTGAGAGAG//SEQ ID NO:4279
NT2RP2000739//AGCAACAGGGAATGGAGGTG//SEQ ID NO:4280
NT2RP2000818//GGGAAGAAATGAGACAAAGA//SEQ ID NO:4281
NT2RP2001200//ACCACATAGCTGCAGGAAAG//SEQ ID NO:4282
NT2RP2001276//TTGCCGTTGGTGCTGGTAGT//SEQ ID NO:4283
NT2RP2001388//TGGCACAATCTCCGCTCACT//SEQ ID NO:4284
NT2RP2001469//TAATGGGTGGTGGGAGCTGA//SEQ ID NO:4285
NT2RP2001538//GAAAAGGGTAGGCAGCAAGG//SEQ ID NO:4286
NT2RP2001562//CACCCTGCCACAAGACATTT//SEQ ID NO:4287
NT2RP2001662//AAGAGGCTGGGCAAATGGCA//SEQ ID NO:4288
NT2RP2001755//CAAGCAAATAATCCAGCCAT//SEQ ID NO:4289
NT2RP2001817//CTAAAGCAACACAGGAATAC//SEQ ID NO:4290
NT2RP2001921//TGTGGGGTTGGTCTTTGGAA//SEQ ID NO:4291
NT2RP2001948//GCATTGAGGACTTTTCCAGA//SEQ ID NO:4292
NT2RP2002015//GTAGTTCTCTCTGAAGAATC//SEQ ID NO:4293
NT2RP2003138//ATGGAAGAGGCTGAGGCAAA//SEQ ID NO:4294
NT2RP2003194//CACCTCTCATGTTTCTGCAC//SEQ ID NO:4295
NT2RP2003302//AGAGGACAGTTGGAAGATTT//SEQ ID NO:4296
NT2RP2003390//CTGTGGGTGATTTCTGGCA//SEQ ID NO:4297
NT2RP2003693//CTGACCCCTAAGTAAATGAA//SEQ ID NO:4298
NT2RP2003664//GGGTGTGATGTTTACTTCTC//SEQ ID NO:4299
NT2RP2003950//CTGAAGGAGGTACTGACACT//SEQ ID NO:4300
NT2RP2004069//CATCACCAAGGTATTAAGCC//SEQ ID NO:4301
NT2RP2004103//GATAGGTTACTGGTGAATTG//SEQ ID NO:4302
NT2RP2005069//GAAAATGAACCTGTAGCCTT//SEQ ID NO:4303
NT2RP2005378//ATTCTGGCTCCCTCTTCCTC//SEQ ID NO:4304

NT2RP2005391//CAAGGTGGATTTACATGGG//SEQ ID NO:4305
NT2RP2005535//GAATTATCGCCATGTCTCTT//SEQ ID NO:4306
NT2RP2005597//GACCAAGACCCTTCAACCTC//SEQ ID NO:4307
NT2RP2006092//TCCTACGTTGTGGTGCAGTG//SEQ ID NO:4308
NT2RP2006134//TGACTGCCAATTAGAAACCT//SEQ ID NO:4309
NT2RP2006208//AAAATTGGCTTCTGCCTAGT//SEQ ID NO:4310
NT2RP2006476//GTTCACCTTCACATCCAAAA//SEQ ID NO:4311
NT2RP3000011//TGGCACAATCTCAGCTCACT//SEQ ID NO:4312
NT2RP3000031//TTCTGGGCTGGAGTAGTGGT//SEQ ID NO:4313
NT2RP3000063//AGATAGTCACATAGACAGAG//SEQ ID NO:4314
NT2RP3000125//ACACATCCAACCCTTCACTT//SEQ ID NO:4315
NT2RP3000148//AACAAGTCCAGCCCCAGAAG//SEQ ID NO:4316
NT2RP3000169//CCAAGCACGCCATATGAAGC//SEQ ID NO:4317
NT2RP3000171//CAGAATTTTGCCACGAGGAT//SEQ ID NO:4318
NT2RP3000172//GGCACAGACACCATCCTTGA//SEQ ID NO:4319
NT2RP3000201//AATGGGGTTTTGCCAGGTTG//SEQ ID NO:4320
NT2RP3000232//ACCTTCATACAACTTTTCCC//SEQ ID NO:4321
NT2RP3000304//TGGTCTGCCTCATCCTTCTC//SEQ ID NO:4322
NT2RP3000378//GAAAAGGGTAGGCAGCAAGG//SEQ ID NO:4323
NT2RP3000427//ATGTAAAGTGTGGAGTACCC//SEQ ID NO:4324
NT2RP3000444//TTCTTCTCAGTCACCTCCAC//SEQ ID NO:4325
NT2RP3000616//GTGATAGTAACACAATCCTG//SEQ ID NO:4326
NT2RP3000645//TGGCCAGTGTATGAGAGGTC//SEQ ID NO:4327
NT2RP3000676//CAAGACAACAAAACAGAAGG//SEQ ID NO:4328
NT2RP3000677//TCCATTTTAGCTGTAGACAC//SEQ ID NO:4329
NT2RP3000721//GAGACTGTGATGCCTTGGTG//SEQ ID NO:4330
NT2RP3000789//AACTGATGGCTTCTGTCTCC//SEQ ID NO:4331
NT2RP3000818//GGGAGAAGCCTAGAAAAGAA//SEQ ID NO:4332
NT2RP3000820//TCACATTCAAGCTCTACGTC//SEQ ID NO:4333
NT2RP3000838//CTAGCTTCCTCTCCCAACTG//SEQ ID NO:4334
NT2RP3000871//GATTGTGCTTGGAGCTTGGC//SEQ ID NO:4335
NT2RP3000907//GGGAGATGAAGAGGAAGCAG//SEQ ID NO:4336
NT2RP3000921//ACATGGGTAGCACTCCTTTT//SEQ ID NO:4337
NT2RP3001012//ACCCATTTCTACCTCTCTTA//SEQ ID NO:4338
NT2RP3001044//AGCAAGGCAATGAGGATACT//SEQ ID NO:4339
NT2RP3001159//AAATGTAGGGGTGGGGAAGT//SEQ ID NO:4340
NT2RP3001240//AGCAAGGTCTCCAGAGTGTG//SEQ ID NO:4341
NT2RP3001271//GTGCTTCTACCATTGAGGAT//SEQ ID NO:4342
NT2RP3001542//TGGTCCTCACTGCCTTCAAA//SEQ ID NO:4343

NT2RP3001560//GGCCTCCACAAACAAACCCT//SEQ ID NO:4344
NT2RP3001592//TAAAAGGGAGGATGTTCAGT//SEQ ID NO:4345
NT2RP3001650//GCATCTTCTGGTAGTTGTCC//SEQ ID NO:4346
NT2RP3001685//GATTCTCCTTGCCTCAGCCT//SEQ ID NO:4347
NT2RP3001754//AGTTAGTGGTGCCTGCTTCC//SEQ ID NO:4348
NT2RP3001976//CTCACTGGCATTTAGCTGGT//SEQ ID NO:4349
NT2RP3002015//CAACAACCTTCCTCCTACCC//SEQ ID NO:4350
NT2RP3002281//TAAACAGTCAACCAATGCTC//SEQ ID NO:4351
NT2RP3002286//AAGCAAGAGATTTGGAGGAA//SEQ ID NO:4352
NT2RP3002353//GGCTGGAACTCAATTTCTGC//SEQ ID NO:4353
NT2RP3002409//GTACCCCTAGTGAAGACCTG//SEQ ID NO:4354
NT2RP3002411//TCAATAGCTACCTGTAGAGT//SEQ ID NO:4355
NT2RP3002448//TCTTCCTACGACATAACCAT//SEQ ID NO:4356
NT2RP3002571//GCCCAAAATCCAACAGTAAA//SEQ ID NO:4357
NT2RP3002721//AGTGGCTTGTATTCTGTGGA//SEQ ID NO:4358
NT2RP3002737//GTGAGGTACTTGCATATCCG//SEQ ID NO:4359
NT2RP3002738//TCCCCGATGAACACCAGCTT//SEQ ID NO:4360
NT2RP3002790//CTGGAGCCTGATTATGAGAA//SEQ ID NO:4361
NT2RP3002836//CTTTAGCAACATAACCTCCA//SEQ ID NO:4362
NT2RP3002900//TTTCTTCCTCCCTAACACAT//SEQ ID NO:4363
NT2RP3002958//GCCTTCTTCCAGCTCTACAT//SEQ ID NO:4364
NT2RP3002983//AATTTCCTTGCTAGAAGGCT//SEQ ID NO:4365
NT2RP3003354//GGCTGACACCTATTATCCCA//SEQ ID NO:4366
NT2RP3003448//TGTAGTCCCAGCTATTCAGG//SEQ ID NO:4367
NT2RP3003473//AATTAATCTCTGGGTAGCAC//SEQ ID NO:4368
NT2RP3003527//TGTCAATGGCCAGGTCGTAG//SEQ ID NO:4369
NT2RP3003532//TAAACTGACTTCCTCTTGGG//SEQ ID NO:4370
NT2RP3003535//CTAATGCCAGTGTTTCAAGA//SEQ ID NO:4371
NT2RP3003559//AATTCTTGTCCTGCTTTTGC//SEQ ID NO:4372
NT2RP3003614//GGGTCTTTGGATTGAGTGTC//SEQ ID NO:4373
NT2RP3003963//CACGATTATCTCTGCCAAAA//SEQ ID NO:4374
NT2RP3004000//TGGCCAGTGTATGAGAGGTC//SEQ ID NO:4375
NT2RP3004025//CACATTCTGGTGGAAAAGCA//SEQ ID NO:4376
NT2RP3004067//TGATGACACGCAGCACTTCC//SEQ ID NO:4377
NT2RP3004075//TTTCAAGTCAACACCTGCAC//SEQ ID NO:4378
NT2RP3004090//TACACTACAGATGGGCAAAA//SEQ ID NO:4379
NT2RP3004119//TCTAAGGCTGGGTACAGTGG//SEQ ID NO:4380
NT2RP3004130//ACATTTCTCCTCCATACGCA//SEQ ID NO:4381
NT2RP3004133//TAACCGCACTATGAGGAAAG//SEQ ID NO:4382

NT2RP3004202//CAGTGGCCTGGTAATAGAGT//SEQ ID NO:4383
NT2RP3004294//ATATTCCACTCCCCATTCGG//SEQ ID NO:4384
NT2RP3004321//GACCAACATGCTAGAAGTGC//SEQ ID NO:4385
NT2RP3004345//AACTCTCATTCCATAAGGTG//SEQ ID NO:4386
NT2RP3004406//CACCTAAAAGACTAATCCCT//SEQ ID NO:4387
NT2RP3004552//GAATCCAAAAGCCGGTAGGG//SEQ ID NO:4388
NT2RP3004557//GAAAGAGGTCAAAGTACCTG//SEQ ID NO:4389
NT2RP3004625//ATACAGGCAGCAGGAATCAC//SEQ ID NO:4390
NT2RP3004647//CAAGACAACAAAACAGAAGG//SEQ ID NO:4391
NT2RP4000634//ATGAAGAGTTACCTATGTGG//SEQ ID NO:4392
NT2RP4000962//AACCCTGGGCTTGGAATTCA//SEQ ID NO:4393
NT2RP4001001//TTTCACAATGCTACAGAGGT//SEQ ID NO:4394
NT2RP4001009//AATGTCAGCGGAGCAAAAGA//SEQ ID NO:4395
NT2RP4001467//GTTGAGAATGCTGGACTTGA//SEQ ID NO:4396
NT2RP4001877//AATCATATAGTCCCAGGTTG//SEQ ID NO:4397
NT2RP4001879//GTGTGAGAGTAGTTGGGGAA//SEQ ID NO:4398
NT2RP4002187//TCAATAGCTACCTGTAGAGT//SEQ ID NO:4399
NT2RP4002451//CATAAACAGTGACAGCAGAA//SEQ ID NO:4400
NT2RP4002715//AGCAAGGCAATGAGGATACT//SEQ ID NO:4401
NT2RP4002750//CAGCATTTAGGTGTGACGAT//SEQ ID NO:4402
PLACE1000040//ACATTGCTTGAGTCTTGCCA//SEQ ID NO:4403
PLACE1000986//CAAGGAGGTAATAGGGAGAT//SEQ ID NO:4404
PLACE1002080//CTCACTCTGTCATCGAGGCT//SEQ ID NO:4405
PLACE1002547//GTACCCCTAGTGAAGACCTG//SEQ ID NO:4406
PLACE1002911//CAAAGGCAAGTGTTCAGGCT//SEQ ID NO:4407
PLACE1003407//GACTACAAAACCCTGGAAAG//SEQ ID NO:4408
PLACE1003573//GGTGGCATGTAAATAAGACT//SEQ ID NO:4409
PLACE1004078//CTCAGCCTTCCAAGTAGCAG//SEQ ID NO:4410
PLACE1004199//GGAATCTGGGAGTCAAAATC//SEQ ID NO:4411
PLACE1004305//GCACCACTTTCGTCTTGAGC//SEQ ID NO:4412
PLACE1004450//GGCACTTAGCTTCTTGTTTT//SEQ ID NO:4413
PLACE1004492//TGGGCATCAATAAACACCTC//SEQ ID NO:4414
PLACE1004630//TGCTTTTGTATGGCCTGGGA//SEQ ID NO:4415
PLACE1004816//ATGTGGACAGGCAAGCAGAG//SEQ ID NO:4416
PLACE1005031//GGTGTTCCCCTTCTTGTTTG//SEQ ID NO:4417
PLACE1005539//AGAGGTAGAATGAGGGGAAA//SEQ ID NO:4418
PLACE1005569//CTGAACCCTGGCCTGTGAAA//SEQ ID NO:4419
PLACE1005601//AGATGGGGACTATGAAGAGG//SEQ ID NO:4420
PLACE1005735//CCTGTAATCCCAGCACTTTG//SEQ ID NO:4421

PLACE1005815//AGAGACAGAGTTTTGCTCTT//SEQ ID NO:4422
PLACE1005927//GGTGTAGCCCATTGTAGAGG//SEQ ID NO:4423
PLACE1006071//TTTGCTCTTTAACTCTGCCT//SEQ ID NO:4424
PLACE1006073//TAAAGGGCAGGGTGGAGGAA//SEQ ID NO:4425
PLACE1006079//TGATGTCCACTGTCTTATTG//SEQ ID NO:4426
PLACE1006786//CAAGGAGGTAATAGGGAGAT//SEQ ID NO:4427
PLACE1007077//ATGTGCTGGTAAGTGAAATC//SEQ ID NO:4428
PLACE1007081//GCCGGCCAAGTTTACACGAA//SEQ ID NO:4429
PLACE1007845//TAACCGCACTATGAGGAAAG//SEQ ID NO:4430
PLACE1007971//GACAATTCAACTGGAAGACC//SEQ ID NO:4431
PLACE1008282//CGTGATGACTGCCAACTCCA//SEQ ID NO:4432
PLACE1008359//AACAGGGTCCCATTTATTTG//SEQ ID NO:4433
PLACE1008469//TTGTCATCCTCCTGCCTCTG//SEQ ID NO:4434
PLACE1008657//CTCAGCCTTCCAAGTAGCAG//SEQ ID NO:4435
PLACE1008744//TAAACAAGACCCAGCACCAT//SEQ ID NO:4436
PLACE1008984//TCGAGACCGCTTCCCATAGA//SEQ ID NO:4437
PLACE1009546//AGGTAGCCGATGACAAAGCC//SEQ ID NO:4438
PLACE1010011//GGATATAAAGACAAGGATGC//SEQ ID NO:4439
PLACE1010713//TCAATAGCTACCTGTAGAGT//SEQ ID NO:4440
PLACE1011019//AAGCAGTGAAGCTCCATGCC//SEQ ID NO:4441
PLACE1011116//CCATTACAAACCCTTTAACC//SEQ ID NO:4442
PLACE1011181//TGTTATCCATTGTTCACCTG//SEQ ID NO:4443
PLACE1011364//TGTTGACGCTGATTTAGGCA//SEQ ID NO:4444
PLACE3000213//TAAACAAGACCCAGCACCAT//SEQ ID NO:4445
PLACE4000354//TAAACAAGACCCAGCACCAT//SEQ ID NO:4446
PLACE4000455//CAAGGAGGTAATAGGGAGAT//SEQ ID NO:4447
SKNMC1000014//CGAGACAGGGTCTTGGTTTG//SEQ ID NO:4448
SKNMC1000082//TTTCCTTCGGCTGGTATGGC//SEQ ID NO:4449
Y79AA1000030//TCCTACGTTGTGGTGCAGTG//SEQ ID NO:4450
Y79AA1000037//AGCACCCCTTATTGGAAGAT//SEQ ID NO:4451
Y79AA1000127//GATGCTTACTCCTCTTTGGT//SEQ ID NO:4452
Y79AA1000226//TGCTGATGCCTCTGTTCCCT//SEQ ID NO:4453
Y79AA1000270//GAAACAACCAAGCACCCCAT//SEQ ID NO:4454
Y79AA1000750//ATAAGGGCAGCTGGGAAGTG//SEQ ID NO:4455
Y79AA1000776//TGTTAGTAGCAGGAGGAAGC//SEQ ID NO:4456
Y79AA1000777//ACAGAGTTCAGTCCCCTTTA//SEQ ID NO:4457
Y79AA1000876//GTTAGAGGACACTGGCATCA//SEQ ID NO:4458
Y79AA1000888//ACTGACTTGAGGAATAAGCC//SEQ ID NO:4459
Y79AA1000959//ACACTGAGAGCATGGGAGGT//SEQ ID NO:4460

Y79AA1000967//GGCACAGACACCATCCTTGA//SEQ ID NO:4461
Y79AA1001056//ACAAATGAGCCTGAAAAGTC//SEQ ID NO:4462
Y79AA1001062//TGGTCCTCACTGCCTTCAAA//SEQ ID NO:4463
Y79AA1001090//AGTGCCCTCAAAGCTCCAGT//SEQ ID NO:4464
Y79AA1001212//ACGAAAGCACTCAAATGTCA//SEQ ID NO:4465
Y79AA1001272//GAATGAAATGTGGTTGAGCA//SEQ ID NO:4466
Y79AA1001426//AATGATTCGGGGCAGCAGGA//SEQ ID NO:4467
Y79AA1001427//GAGAGAGACACACACAGAAA//SEQ ID NO:4468
Y79AA1001523//AGTTTTATACCAGCATTGGC//SEQ ID NO:4469
Y79AA1001530//GGTGTAGAAGTAAAATGGGA//SEQ ID NO:4470
Y79AA1001592//GATTGTGTTCTCTTACTCCT//SEQ ID NO:4471
Y79AA1001727//GCTCCACCTGACGTTCTTTA//SEQ ID NO:4472
Y79AA1001795//GTCTCCCATATCGCTGTCTT//SEQ ID NO:4473
Y79AA1001803//CACTTTCTAATAACCCTTGG//SEQ ID NO:4474
Y79AA1001863//TTGGGATTGGAAACCGCATT//SEQ ID NO:4475
Y79AA1001874//AGAAACCACTGAGGCCCAAG//SEQ ID NO:4476
Y79AA1002058//CAGAAGCAGAAGCAGGAGCA//SEQ ID NO:4477
Y79AA1002121//ATTTACTGCGATTTCTCCTG//SEQ ID NO:4478
Y79AA1002129//GAGTTTCTTTGCTAGTTCCA//SEQ ID NO:4479
Y79AA1002334//ATATTTGTGTTTGCCTTGGG//SEQ ID NO:4480
Y79AA1002373//GGATGGCTGGGTCAAATGGT//SEQ ID NO:4481
Y79AA1002376//AATGATGGCTAGGGTGACTT//SEQ ID NO:4482
Y79AA1002378//TCTTCCCACATTCGTTACAC//SEQ ID NO:4483
Y79AA1002381//AGGGAGTAGATGTTGGTAAA//SEQ ID NO:4484

[0279] The result of expression frequency analysis is shown in Table 367. Only clones with correlation coefficient of 0.9 or higher are indicated in this Table. Clones that are not presented in the Table include clones for which the assay could not performed because of low expression levels thereof in internal standard samples or because of unexpectedly smaller or larger sizes of the PCR products.

[0280] Among the clones that could be analyzed, clones of which expression levels increased by two fold in response to the IL-1. stimulation 1 or 7 hours after the stimulation are: NT2RM2000514, NT2RP3001159, MAMMA1001237 and MAMMA1000614.

[0281] Clones of which expression levels increased by two fold in response to the TNF-stimulation 1, 3 or 7 hours after the stimulation are:

NT2RM2000582, NT2RM2002109, NT2RP1000679, NT2RP2003664, NT2RP2005597, NT2RP2004108, NT2RP3001592, NT2RP3002738, NT2RP3004133, NT2RP3004321, NT2RP3004557, NT2RP3004294, MAMMA1001237, MAMMA1000141, MAMMA1000788, MAMMA1002070, PLACE1002547, PLACE1003573, PLACE1004305, PLACE1008744, PLACE1011181, PLACE1010713, PLACE1010011, Y79AA1000776, Y79AA1002129,

[0282] Among the clones of which expression levels increased in response to IL-1. stimulation, MAMMA1001237 was a clone of which expression level was varied in response to TNF-. stimulation. Among clones showing higher expression levels (with relative value of 5 or higher) prior to the stimulation, PLACE1002080 is an example of clones

of which expression was suppressed by the stimulation. The expression of the clone decreased by three or more fold in response to the stimulation. These genes were found to be associated with inflammatory reaction induced by IL-1. or TNF-..

[0283] In Example 15, the genes of which expression levels were varied by culturing in the presence of TNF-. were analyzed by hybridization with high-density DNA filter. As for 3 clones (NT2RP3004557, NT2RP3004294 and PLACE 1002547), the results obtained by ATAC-PCR method were similar to those obtained by hybridization method. However, the results obtained by ATAC-PCR method were not necessarily consistent with those obtained by the hybridization method. Possible reasons for the inconsistency are the difference in cells used between the two experiments, unavailability of some data in the ATAC-PCR experiment, and the difference in the method of data treatment.

Table 28

Expression of each cDNA in human tissues (The Table also contains clones with no description in Examples)

Clone_name	Heart	Lung	P.gland	Thymus	Brain	Kidney	Liver	Spleen
GAPDH(Cr1)	38.210	32.670	23.820	13.580	11.230	21.120	24.910	22.440
βactin(Cr2)	279.280	368.870	111.100	117.500	92.880	114.650	82.990	256.790
ADRGL1000005	53.882	23.005	32.749	22.858	26.564	24.940	22.644	27.001
ADRGL1000007	94.778	85.185	160.457	67.191	101.768	62.489	67.150	73.543
ADRGL1000009	11.141	50.520	10.357	7.177	6.013	5.219	14.272	21.225
ADRGL1000011	71.656	24.579	29.358	19.473	24.898	30.747	49.220	22.221
ADRGL1000027	36.238	25.252	20.855	7.328	11.196	14.298	19.658	11.288
ADRGL1000058	66.209	129.497	55.226	49.241	30.219	55.872	67.027	243.436
ADRGL1000069	38.630	23.459	28.991	12.540	27.353	33.633	28.774	20.911
ADRGL1000077	97.465	63.656	448.427	83.412	71.108	53.740	67.906	89.439
ADRGL1000092	89.423	45.692	55.810	26.033	44.148	73.339	96.037	73.091
ADRGL1000099	73.675	24.424	36.128	17.024	25.964	41.391	42.837	29.666
ADRGL1000136	141.745	63.974	77.017	24.777	33.549	58.986	295.009	84.985
ADRGL1000147	394.563	155.829	271.210	92.899	165.627	251.266	253.420	150.294
ADRGL1000159	50.073	25.425	39.296	15.194	16.125	20.040	33.720	23.278
ADRGL1000160	69.386	31.051	59.416	20.154	39.799	27.027	47.169	20.716
ADRGL1000171	57.047	23.011	43.063	23.860	40.581	59.814	117.055	32.630
ADRGL1000181	45.892	18.666	34.476	15.434	34.225	32.962	39.693	16.334
BGGI11000015	153.242	42.337	92.865	41.003	45.168	88.524	85.990	73.392
BGGI11000016	177.367	94.731	119.688	34.159	30.249	98.806	98.783	39.204
BGGI11000017	84.712	32.614	38.131	20.878	18.769	32.340	39.666	20.750
BGGI11000022	52.468	20.452	67.167	12.167	11.158	18.241	19.197	11.937
BGGI11000031	30.008	17.072	40.883	12.585	13.313	15.525	16.757	13.406
BGGI11000042	49.926	36.336	51.176	26.964	43.122	43.770	49.107	38.776
BGGI11000046	31.618	26.472	34.182	31.854	12.650	25.784	18.430	25.385
BNGH41000020	5031.103	2993.496	1444.841	537.162	5973.542	6029.124	3350.527.	3649.144
BNGH41000025	91.717	35.026	73.901	27.713	30.765	36.523	37.596·	47.074
BNGH41000026	176.757	77.439	98.345	35.807	56.991	91.310	75.797	70.241
BNGH41000027	65.029	56.353	25.896	22.494	12.763	23.748	17.836	23.859
BNGH41000035	148.779	66.776	119.727	56.576	60.996	96.959	72.461	64.458
BNGH41000037	79.500	29.611	43.438	18.317	20.857	36.272	27.525	24.771
BNGH41000042	224.484	110.084	168.448	104.351	102.259	125.323	86.783	122.959
BNGH41000048	56.144	32.253	54.063	14.729	27.312	22.435	29.566	28.937
BNGH41000056	67.258	18.694	30.075	15.602	10.072	20.735	16.100	7.642
BNGH41000087	98.262	46.173	77.657	35.329	40.900	50.029	50.841	45.285
BNGH41000091	50.895	16.985	28.392	10.147	5.469	22.794	10.725	12.410
BNGH41000157	69.043	34.730	40.597	18.088	27.072	22.074	25.410	24.950
BNGH41000169	44.850	21.770	28.655	11.403	25.991	28.509	25.634	25.843
BNGH41000181	17.163	15.689	13.948	3.996	9.287	13.139	15.553	16.575
BNGH41000198	81.510	36.250	60.860	20.585	26.929	35.751	31.695	28.325
BNGH41000219	30.302	25.156	22.187	13.757	11.208	15.235	27.285	35.709
BNGH41000229	252.790	65.948	93.499	51.108	92.555	101.245	96.716	78.266
BNGH41000237	85.757	46.997	55.170	26.780	33.764	47.456	37.007	39.131
BNGH41000238	17.744	36.938	42.360	14.922	35.749	42.848	39.238	13.241
BNGH41000243	45.446	23.667	44.798	20.875	10.516	23.918	22.443	27.033
BNGH41000270	60.889	18.651	29.618	10.724	15.979	12.351	19.152	22.314
BRAWH1000004	43.673	28.539	7.640	11.388	19.198	14.903	32.353	23.777
BRAWH1000018	59.409	17.941	102.270	17.107	709.078	25.732	24.214	24.767
BRAWH1000021	104.772	29.951	51.142	21.042	1169.154	55.762	66.754	27.969
BRAWH1000027	152.205	47.310	67.089	32.199	64.521	70.731	79.670	40.928
BRAWH1000029	106.376	49.221	55.840	40.856	59.552	56.487	64.886	100.132
BRAWH1000040	29.419	16.761	31.101	16.622	30.633	18.200	17.998	15.196
BRAWH1000050	161.264	71.786	118.976	51.863	61.542	97.720	81.271	69.194
BRAWH1000051	74.067	34.341	44.047	20.726	30.434	42.055	53.856	24.624
BRAWH1000060	68.789	22.598	35.012	16.493	19.127	38.662	34.923	28.094
BRAWH1000075	17.318	16.898	36.437	8.901	18.133	17.219	9.321	11.200
BRAWH1000081	43.025	12.998	28.267	7.655	123.677	17.673	15.924	9.844
BRAWH1000084	174.384	42.178	80.534	47.752	152.188	77.111	110.167	102.296
BRAWH1000095	118.239	59.676	64.528	28.174	116.975	53.814	746.700	35.985
BRAWH1000096	145.112	44.967	85.882	27.491	145.013	52.880	52.427	58.678
BRAWH1000097	95.841	72.506	174.954	65.637	64.200	73.707	63.827	63.762
BRAWH1000100	11.943	19.037	18.950	13.536	92.145	16.582	16.646	10.218
BRAWH1000101	134.838	57.232	106.632	40.741	96.396	71.642	88.432	57.336

NASE I).//1.00E-77//359aa//44%//Q14012
C-Y79AA1001013
C-Y79AA1001056//Homo sapiens MAID protein mRNA, complete cds.//0//1475bp//99%//AF113535
C-Y79AA1001062//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//8.90E-12//132aa//38%//Q13829
C-Y79AA1001090//NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) (NF-KAPPA-B1 P84 /NF-KAPPA-B1 P98) [CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT] (FRAGMENT).//4.50E-09//144aa//31%//Q63369
C-Y79AA1001212//Homo sapiens SL15 protein mRNA, complete cds.//6.30E-306//1388bp//99%//AF038961
C-Y79AA1001264//HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.//5.10E-106//351aa//58%//Q10005
C-Y79AA1001272//Homo sapiens retinoic acid repressible protein (RARG-1) mRNA, complete cds.//1.50E-183//867bp//98%//AF172066
C-Y79AA1001328//Mus musculus mRNA for Dll3 protein, complete cds.//1.90E-263//1988bp//79%//AB013440
C-Y79AA1001426//ANION EXCHANGE PROTEIN 3 (CARDIAC/BRAIN BAND 3-LIKE PROTEIN) (CAE3/BAE3).//6.20E-66//609aa//31%//P48751
C-Y79AA1001427//Homo sapiens cytochrome b5 reductase 1 (B5R.1) mRNA, complete cds.//0//1588bp//99%//AF169481
C-Y79AA1001430//Homo sapiens mRNA for KIAA0469 protein, complete cds.//0//2943bp//99%//AB007938
C-Y79AA1001523//Homo sapiens transcriptional intermediary factor 1 alpha mRNA, complete cds.//0//2263bp//99%//AF119042
C-Y79AA1001530//Human beta-tubulin gene (5-beta) with ten Alu family members.//0//1920bp//98%//X00734
C-Y79AA1001592
C-Y79AA1001727//CELL SURFACE A33 ANTIGEN PRECURSOR.//1.10E-13//286aa//27%//Q99795
C-Y79AA1001787//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//1.70E-133//544aa//37%//Q12697
C-Y79AA1001793//Mus musculus mRNA for GSG1, complete cds.//3.70E-126//532bp//78%//D87325
C-Y79AA1001795//Homo sapiens mRNA for GalT4 protein.//2.30E-250//1137bp//99%//Y15061
C-Y79AA1001799//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//3.40E-54//182aa//39%//P23500
C-Y79AA1001803//Homo sapiens secretogranin III mRNA, complete cds.//0//1871bp//99%//AF078851
C-Y79AA1001863
C-Y79AA1002022//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR.//2.20E-06//140aa//26%//P32507
C-Y79AA1002058//Mus musculus Gng3lg mRNA, complete cds.//4.10E-167//1145bp//83%//AF069954
C-Y79AA1002121//HISTONE H1.//4.90E-12//114aa//35%//P35060
C-Y79AA1002129
C-Y79AA1002213//HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.//1.20E-98//262aa//41%//Q03567
C-Y79AA1002334//GLUCOSE REPRESSION MEDIATOR PROTEIN.//1.70E-10//333aa//23%//P14922
C-Y79AA1002373//Mus musculus mRNA for GSG1, complete cds.//7.20E-147//680bp//79%//D87325
C-Y79AA1002376//Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds.//1.50E-304//1667bp//90%//U39045
C-Y79AA1002378//Homo sapiens zinc finger protein NY-REN-21 antigen mRNA, partial cds.//0//963bp//99%//AF155100
C-Y79AA1002381//Homo sapiens cell cycle related kinase mRNA, complete cds.//0//1791bp//98%//AF035013

Claims

1. Use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-829 and 2545, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides.

2. A primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-829 and 2545, wherein said oligonucleotide comprises at least 15 nucleotides.

3. A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide com-

prising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence.3'-end nucleotide sequence is selected from the group consisting of:

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SEQ ID NO:828 and SEQ ID NO:1571
SEQ ID NO:829 and SEQ ID NO:1572, and
SEQ ID NO:2545 and SEQ ID NO:2546

4. A polynucleotide which can be synthesized with the primer set of claim 2 or 3.

5. A polynucleotide comprising a coding region in the polynucleotide of claim 4.

6. A substantially pure protein encoded by polynucleotide of claim 4.

7. A partial peptide of the protein of claim 6.

8. An isolated polynucleotide selected from the group consisting of

(a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the following SEQ ID NOs:

SEQ ID NO:2547, SEQ ID NO:nnnn , SEQ ID NO:2551, SEQ ID NO:2553, SEQ ID NO:2555, SEQ ID NO:2557, SEQ ID NO:2558, SEQ ID NO:2560, SEQ ID NO:2562, SEQ ID NO:2564, SEQ ID NO:2566, SEQ ID NO:2568, SEQ ID NO:2570, SEQ ID NO:2572, SEQ ID NO:2574, SEQ ID NO:2576, SEQ ID NO:2578, SEQ ID NO:2580, SEQ ID NO:2581, SEQ ID NO:2583, SEQ ID NO:2584, SEQ ID NO:nnnn , SEQ ID NO:2588, SEQ ID NO:2590, SEQ ID NO:2592, SEQ ID NO:2594, SEQ ID NO:2596, SEQ ID NO:2598, SEQ ID NO:nnnn , SEQ ID NO:2602, SEQ ID NO:2604, SEQ ID NO:2606, SEQ ID NO:2607, SEQ ID NO:2609, SEQ ID NO:2611, SEQ ID NO:2613, SEQ ID NO:2615, SEQ ID NO:2617, SEQ ID NO:2619, SEQ ID NO:2621, SEQ ID NO:2623, SEQ ID NO:2625, SEQ ID NO:2627, SEQ ID NO:2629, SEQ ID NO:2630, SEQ ID NO:2632, SEQ ID NO:2634, SEQ ID NO:2636, SEQ ID NO:2638, SEQ ID NO:2640, SEQ ID NO:2642, SEQ ID NO:2644, SEQ ID NO:2646, SEQ ID NO:2648, SEQ ID NO:2650, SEQ ID NO:2652, SEQ ID NO:2654, SEQ ID NO:2656, SEQ ID NO:2658, SEQ ID NO:2660, SEQ ID NO:2662, SEQ ID NO:2664, SEQ ID NO:2666, SEQ ID NO:2668, SEQ ID NO:2670, SEQ ID NO:2672, SEQ ID NO:2674, SEQ ID NO:2676, SEQ ID NO:2678, SEQ ID NO:2680, SEQ ID NO:2681, SEQ ID NO:2683, SEQ ID NO:2685, SEQ ID NO:2686, SEQ ID NO:2688, SEQ ID NO:2690, SEQ ID NO:2692, SEQ ID NO:2694, SEQ ID NO:2696, SEQ ID NO:2698, SEQ ID NO:2700, SEQ ID NO:2702, SEQ ID NO:2704, SEQ ID NO:2706, SEQ ID NO:2708,

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SEQ ID NO:4167, SEQ ID NO:4168, SEQ ID NO:4170, SEQ ID NO:4172, SEQ ID NO:4174, SEQ ID NO:4176, and SEQ ID NO:4178

(b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence

set forth in any one of the following SEQ ID NOs:

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SEQ ID NO:4164, SEQ ID NO:4166
SEQ ID NO:4169, SEQ ID NO:4171, SEQ ID NO:4173, SEQ ID NO:4175, SEQ ID NO:4177, and SEQ ID NO:4179

(c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence selected from the amino acid sequences of (b), in which one or more amino acids are substituted, deleted, inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino acid sequence selected from the amino acid sequences of (b);
(d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the nucleotide sequences of (a), and that comprises a nucleotide sequence encoding a protein functionally equivalent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences of (a);
(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein encoded by the polynucleotide of (a) to (d);
(f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence of (a).

9. A substantially pure protein encoded by the polynucleotide of claim 8.

10. An antibody against the protein or peptide of any one of claims 6, 7, and 9.

11. A vector comprising the polynucleotide of claim 5 or 8.

12. A transformant carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.

13. A transformant expressively carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.

14. A method for producing the protein or peptide of any one of claims 6, 7, and 9, comprising culturing the transformant of claim 13 and recovering the expression product.

15. An oligonucleotide comprising the nucleotide sequence of claim 8 (a) or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.

16. Use of the oligonucleotide of claim 15 as a primer for synthesizing a polynucleotide.

17. Use of the oligonucleotide of claim 15 as a probe for detecting a gene.

18. An antisense polynucleotide against the polynucleotide of claim 8, or the portion thereof.

19. A method for synthesizing a polynucleotide, the method comprising:

a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of claim 2 or 3, or the primer of claim 16; and
b) recovering the synthesized product.

20. The method of claim 19, wherein the cDNA library is obtainable by oligo-capping method.

21. The method of claim 19, wherein the complementary strand is obtainable by PCR.

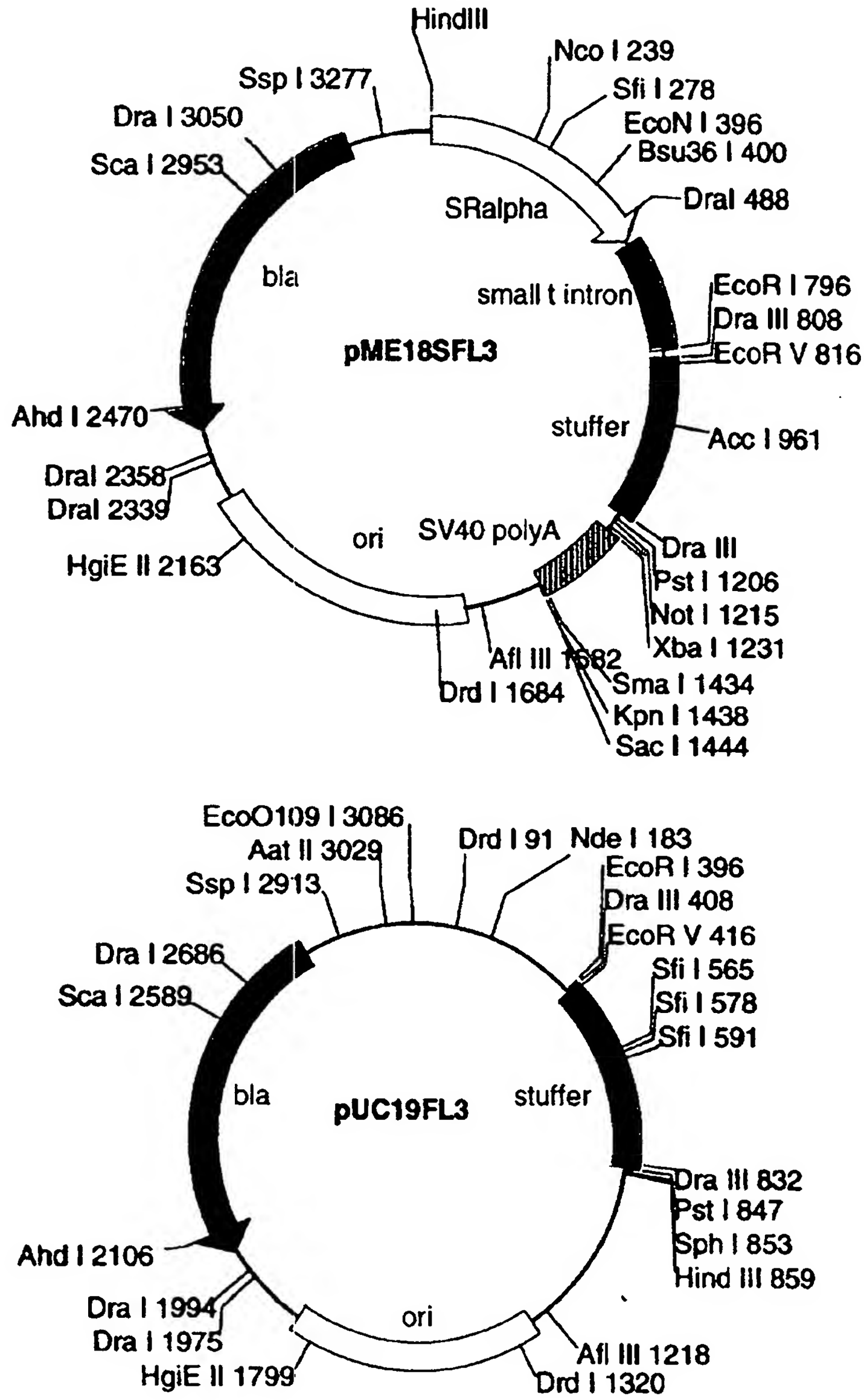
22. A method for detecting the polynucleotide of claim 8, the method comprising:

a) incubating a target polynucleotide with the oligonucleotide of claim 15 under the conditions where hybridization occurs, and
b) detecting the hybridization of the target polynucleotide with the oligonucleotide of claim 15.

23. A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences of claim 8 (a) and/or the amino acid sequences of claim 8 (b), or a medium

on which the database is stored.

Figure 1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Ssp I 3277
Dra I 3050
Sca I 2953
SRalpha
bla
small t intron
EcoR I 796
Dra III 808
EcoR V 816
pME18SFL3
Ahd I 2470
stuffer
Acc I 961
DraI 2358
DraI 2339
ori
SV40 polyA
Dra III
Pst I 1206
Not I 1215
Xba I 1231
HgiE II 2163
AfI III 1682
Drd I 1684
Sma I 1434
Kpn I 1438
Sac I 1444
EcoO109 I 3086
Aat II 3029
Drd I 91
Nde I 183
Ssp I 2913
EcoR I 396
Dra III 408
EcoR V 416
Dra I 2686
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Sfi I 578
Sfi I 591
bla
pUC19FL3
stuffer
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Pst I 847
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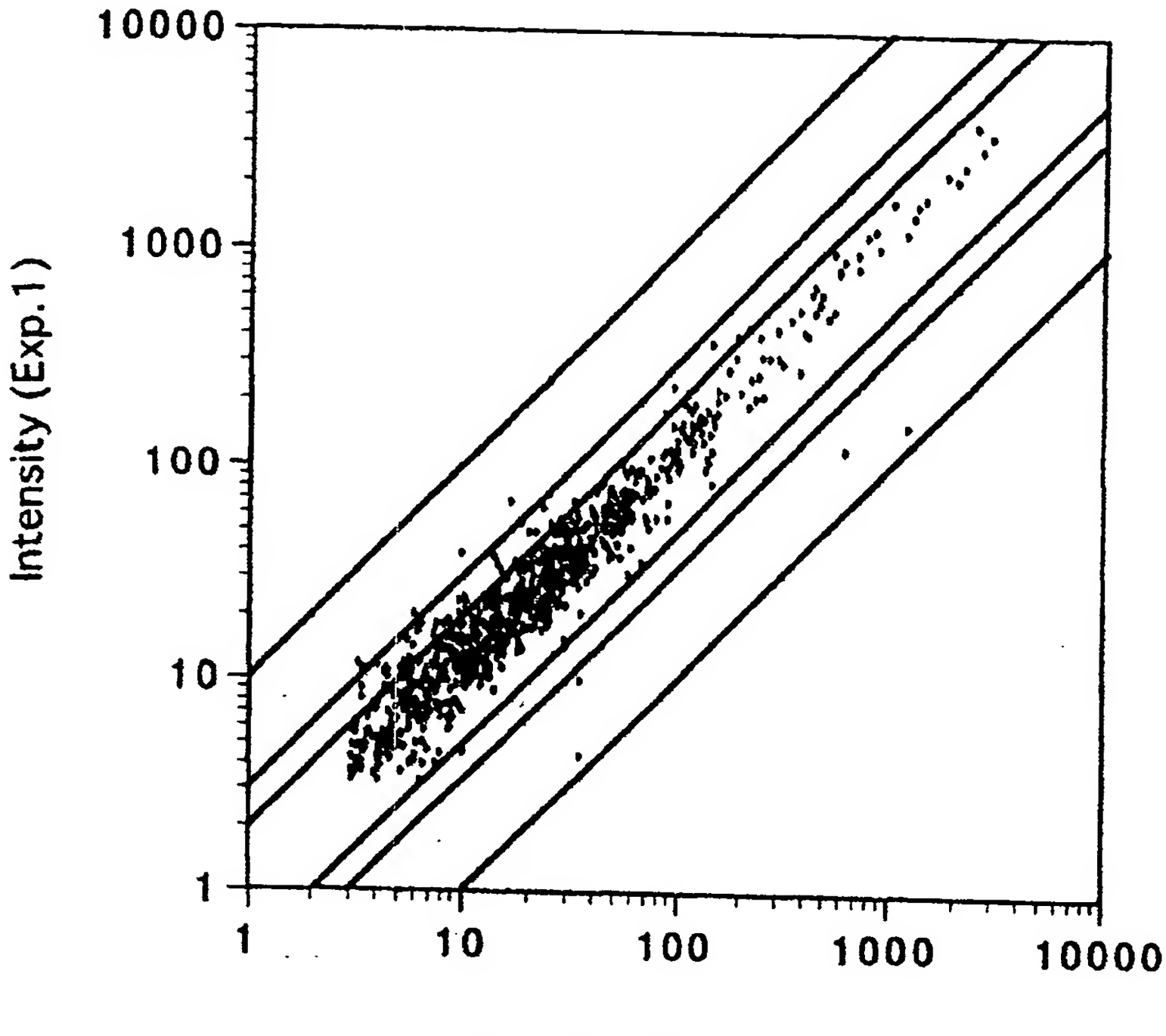
Figure 2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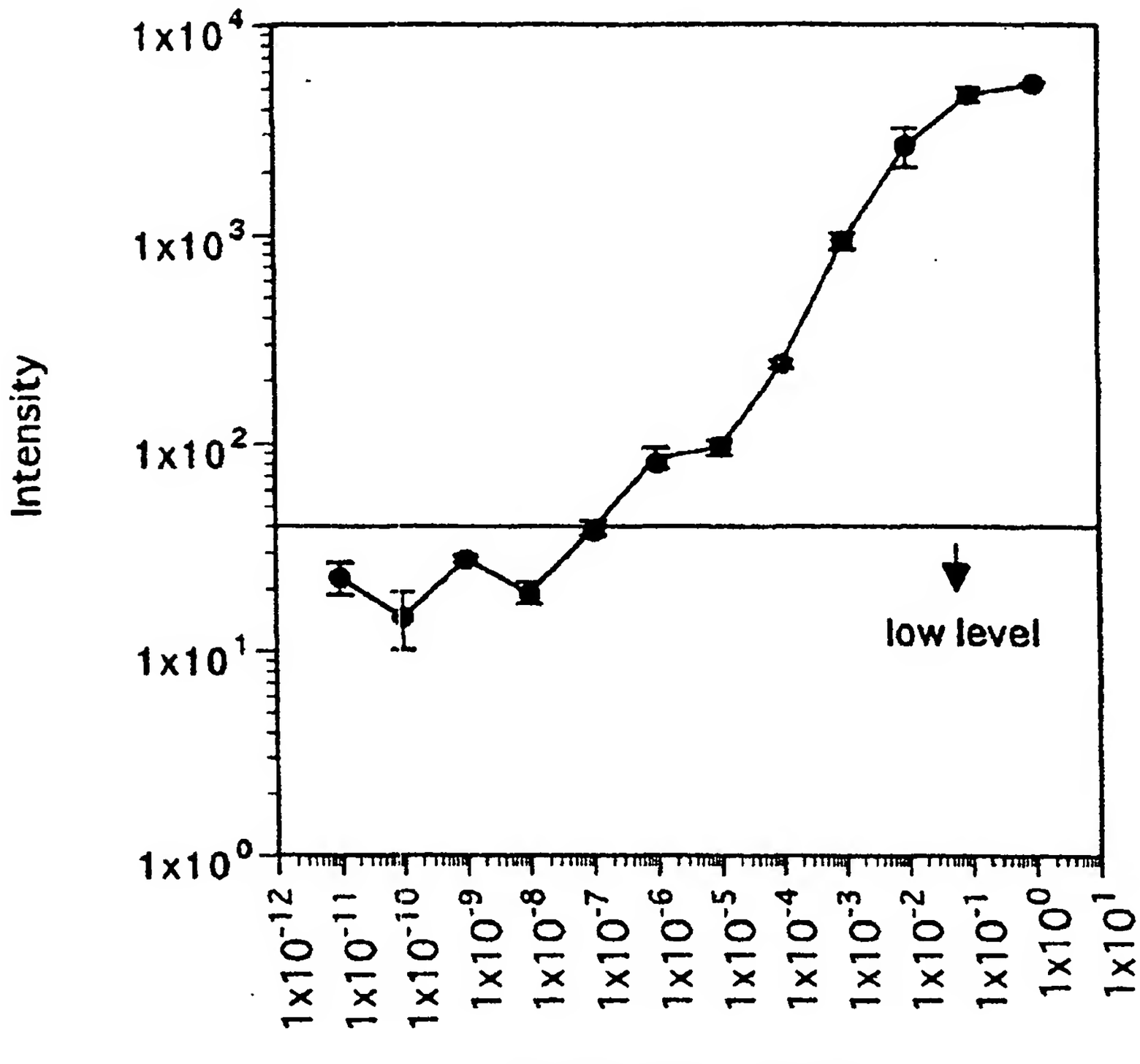
1000
10000
Intensity (Exp. 2)

Figure 3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Probe conc. (μg/ml)